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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:41:34 ; Search time 75 Seconds
(without alignments)
950.521 Million cell updates/sec

Title: US-09-888-035A-2

Perfect score: 2722

Sequence: 1 MGMEVAARALGALYTTSDYA.....GRGFVPSPGSPTEQSHGGR 535

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_101002.*

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2722	100.0	535	21	AA11832
2	2105.5	77.4	555	21	AA12786
3	2103.5	77.3	540	22	AA173252
4	2095.5	77.0	553	22	AA173253
5	2055.5	75.5	542	22	AA173251
6	2023.5	74.3	538	20	AA140901
7	1966	72.2	555	22	AA173254
8	1852.5	68.1	547	20	AA140905
9	1799.5	66.1	571	22	AA102882
10	1550.5	57.0	556	23	AA178424

11	1529	56.2	529	20	AA140902	Arabidopsis thalia
12	618	22.7	671	23	ABG61535	Human transporter
13	600.5	22.1	608	21	AB29621	Cat flea HMT Na/H
14	595.5	21.9	649	22	AB59364	Drosophila melanog
15	565.5	20.8	673	23	AA16770	Human transporter
16	565	20.8	727	22	AB65651	Drosophila melanog
17	552	20.3	569	20	AA14016	Schizosaccharomyce
18	541.5	19.9	509	22	AA190555	Human secreted pro
19	541.5	19.9	509	23	ABG65438	Human albumin fusi
20	541.5	19.9	526	22	AB190637	Human secreted pro
21	539	19.8	631	23	AA141196	Human transporter
22	533	19.6	633	20	AA14017	Saccharomyces cere
23	481	17.7	816	14	AA14143	Rabbit sodium ion/
24	479.5	17.6	834	18	AA11325	Human Na/H+ excha
25	475.5	17.5	518	22	AB58504	Drosophila melanog
26	448	16.5	707	23	AA14204	Human transporter
27	448	16.5	717	23	AA185408	Human protein NOV6
28	439	16.1	325	20	AA140906	Arabidopsis thalia
29	425.5	15.6	605	22	AA102884	Yeast ScNHX1 polyp
30	416.5	15.3	664	22	AA102883	Human HsNHE-6 poly
31	369.5	13.6	273	22	AA101607	Gene #21 human sec
32	362	13.3	275	22	AA101608	Human secreted pro
33	350	12.9	315	22	AA124062	Human EST encoded
34	312	11.5	531	23	AB191666	Herbicideally activ
35	303.5	11.1	359	22	AA101581	Human secreted pro
36	292.5	10.7	339	22	AA190590	Human secreted pro
37	292.5	10.7	339	22	AA190591	Human secreted pro
38	292.5	10.7	339	23	ABG65436	Human albumin fusi
39	292.5	10.7	339	23	ABG65437	Human albumin fusi
40	288	10.6	990	22	ABG29884	Novel human diagno
41	285.5	10.5	1146	23	AA179302	AtNHX transporter
42	284	10.4	707	22	AA123715	Human EST encoded
43	284	10.4	707	22	AA123744	Human EST encoded
44	273	10.0	232	20	AA140907	Arabidopsis thalia
45	252.5	9.3	511	22	AB10934	Novel human diagno

ALIGNMENTS

RESULT 1

AA11832
ID AA11832 standard; Protein: 535 AA.

XX AA11832;

XX 07-NOV-2000 (first entry)

XX Rice Na/H+ antiporter, OsNHX1.

XX OsNHX1; Na/H+ antiporter; sodium/proton antiporter; countertransporter;
XX active transport; rice; transgenic plant; salt-tolerance.

OS Oryza sativa.

PN WO200037644-A1.

XX 29-JUN-2000.

XX 22-DEC-1999; 99WO-JP07224.

XX 22-DEC-1998; 98JP-0365604.

XX (NORU) JAPAN MIN AGRIC FORESTRY & FISHERIES.

XX Fukuda A, Tanaka Y;

XX WPI; 2000-442672/38.

XX N-PSDB; AAA61876.

XX DNA encoding a sodium ion and proton counter-transporter protein of
XX rice origin for production of salt tolerant rice transformants

PS Claim 1a; Fig 1; 43pp; Japanese.
 XX This sequence represents a novel rice Na⁺/H⁺ antiporter
 CC (countertransporter), OSHX1. The invention relates to OSHX1 and
 CC nucleic acids which encode it; vectors, host cells and transgenic plants
 CC containing OSHX1 nucleic acids; recombinant expression of OSHX1; and
 CC antibodies which recognise OSHX1. OSHX1 nucleic acids are useful in the
 CC production of salt tolerant transgenic plants.
 XX
 SQ Sequence 535 AA;
 Query Match 100.0%; Score 2722; DB 21; Length 535;
 Best Local Similarity 100.0%; Pred. No. 8.4e-271;
 Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGMEVAAARLGALYTTSDYASVSVINLFVALLCACIVLGHLEENRWVNESITALLIGLC 60
 DB 1 MGMEVAAARLGALYTTSDYASVSVINLFVALLCACIVLGHLEENRWVNESITALLIGLC 60
 QY 61 TGVVILLMTKGSSHLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGT 120
 DB 61 TGVVILLMTKGSSHLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGT 120
 QY 121 MISFETISIAAIAIFSRMNIPTLDVGDFAIGAIFSDVSVCTLOVNODETPFLYSLVF 180
 DB 121 MISFETISIAAIAIFSRMNIPTLDVGDFAIGAIFSDVSVCTLOVNODETPFLYSLVF 180
 QY 181 GGGVNDATSI VLFNALQNFDLVHIDAAVVLKFLGNFFYFLFSSTFLGVFAGLLSAYIIT 240
 DB 181 GGGVNDATSI VLFNALQNFDLVHIDAAVVLKFLGNFFYFLFSSTFLGVFAGLLSAYIIT 240
 QY 241 KLYIGRHSITDREVALMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTWHNVTESSRVT 300
 DB 241 KLYIGRHSITDREVALMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTWHNVTESSRVT 300
 QY 301 TKHAFATLSFAETFLFYVGMALDIEKWEFASDRPKSGISISILLGLVLIGRAAFV 360
 DB 301 TKHAFATLSFAETFLFYVGMALDIEKWEFASDRPKSGISISILLGLVLIGRAAFV 360
 QY 361 PLSFSLNLTAKAPNEKITWROQVVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMIT 420
 DB 361 PLSFSLNLTAKAPNEKITWROQVVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMIT 420
 QY 421 STITVVFESTVFGMTKPLRLLLPASGHPVTSEPPSPKSLHSPPLTSMOGSDLESTN 480
 DB 421 STITVVFESTVFGMTKPLRLLLPASGHPVTSEPPSPKSLHSPPLTSMOGSDLESTN 480
 QY 481 IVRPSSRLMLTKPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQSHGGR 535
 DB 481 IVRPSSRLMLTKPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQSHGGR 535
 RESULT 2
 AAB12786
 ID AAB12786 standard; Protein; 555 AA.
 XX
 AC AAB12786;
 XX
 XX
 DT 23-NOV-2000 (first entry)
 XX
 DE Atliplex gmelini Na⁺ and H⁺ antiporter protein.
 XX
 KW Atliplex gmelini; Na⁺ plus and H⁺ plus antiporter protein;
 XX Na⁺ and H⁺ antiporter protein; transformed plant; high salt tolerance.
 XX
 OS Atliplex gmelini.
 XX
 PN JP2000157287-A.
 XX
 PD 13-JUN-2000.
 XX
 PF 16-SEP-1999; 99JP-0261606.
 XX

PR 24-SEP-1998; 98JP-0269504.
 XX (SHOK-) SHOKUBUTSU KOGAKU KK.
 PA WPI; 2000-468209/41.
 DR N-PSDB; AAA72926.
 XX
 PT An Na⁺ and H⁺ plus antiporter protein and a gene encoding it -
 PS Disclosure; Page 10-12; 16pp; Japanese.
 XX
 CC The present sequence represents an Na⁺ and H⁺ antiporter protein
 CC isolated from Atliplex gmelini. The Na⁺ and H⁺ antiporter protein and
 CC gene encoding it are useful for the preparation of transformed plants
 CC with high salt tolerance, e.g. for growth in arid land.
 XX
 SQ Sequence 555 AA;
 Query Match 77.4%; Score 2105.5; DB 21; Length 555;
 Best Local Similarity 76.1%; Pred. No. 2.2e-207;
 Matches 410; Conservative 53; Mismatches 61; Indels 15; Gaps 4;
 QY 7 AARLGALYTTSDYASVSVINLFVALLCACIVLGHLEENRWVNESITALLIGLGTGWL 66
 DB 10 SGKMDAL-TTSDHASVSVNMNLFVALLCGCIVIGHLEENRWVNESITALLIGLGTGWL 68
 QY 67 LMTKGSSHLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGTMSISFT 126
 DB 69 LISGKSSHLVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGTLSVFT 128
 QY 127 ISIAAIAIFSRMNIPTLDVGDFAIGAIFSDVSVCTLOVNODETPFLYSLVFGGVN 186
 DB 129 ISLGALSIFKLDIGTLEADYLAIGAIFAATDSVCTLOVNODETPFLYSLVFGGVN 188
 QY 187 DATSIVLNALQNFDLVHIDAAVVLKFLGNFFYFLFSSTFLGVFAGLLSAYIITKLYIGR 246
 DB 189 DATSVVLFNALQSFDLTRIDHRIALQFMGNFLYFLFIASTILGFTGLLSAYIITKLYIGR 248
 QY 247 HSTDREVALMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTWHNVTESSRVTKHAF 306
 DB 249 HSTDREVALMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTWHNVTESSRVTKHAF 308
 QY 307 TLSFTAETFLFYVGMALDIEKWEFASDRPKSGISISILLGLVLIGRAAFVFLSFLS 366
 DB 309 TLSFVAEFLFYVGMALDIEKWEFASDRPKSGISISILLGLVLIGRAAFVFLSFLS 368
 QY 367 NLTKKAPNEKITWROQVVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMITSTITVV 426
 DB 369 NFAKKSQSEKVTFNQOIVTWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMITSTISVV 428
 QY 427 LFSMTVFGMTKPLRLLLPASGH----PVTSEPPSPKSLHSPPLTSMOGSDL----- 475
 DB 429 LFSMTVFGMTKPLRLLLPASGH----PVTSEPPSPKSLHSPPLTSMOGSDL----- 475
 QY 476 ESTT---NIVRPSRLMLTKPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQS 531
 DB 489 EDTTEPRTVIRPSSRLMLNAPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQS 547
 RESULT 3
 AAB73252
 ID AAB73252 standard; Protein; 540 AA.
 XX
 AC AAB73252;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Protein regulating the pH of vacuoles.
 XX
 KW Vacuole pH regulation; flower colour.
 XX
 OS Petunia hybrida.
 XX

PN W0200114560-A1.
XX 01-MAR-2001.
PD 24-AUG-2000; 2000WO-JP05722.
XX 24-AUG-1999; 99JP-0236800.
XX (SUNR) SUNTORY LTD.
XX Iida S, Tanaka S, Inagaki Y;
PI WPI: 2001-191648/19.
DR N-PSDB; AAF75764.
XX Morning glory-originated gene encoding a protein with pH regulation
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture -
XX Example 7; Page 42-45; 68pp; Japanese.
PS The present sequence is a protein, which has vacuolar pH regulatory
XX activities. The protein enables flower colour to be controlled via
CC regulation of the vacuolar pH, colours can range from blue to red in
CC colour spectrum. The protein is useful in controlling flower colour to
CC give new breeds of colourful plants for cut flowers, particularly
CC applicable in horticulture.
XX Sequence 540 AA;
SQ Query Match 77.3%; Score 2103.5; DB 22; Length 540;
Best Local Similarity 77.4%; Pred. No. 3.4e-207;
Matches 404; Conservative 53; Mismatches 62; Indels 3; Gaps 1;
QY 15 TTSYASVVSINLFAVALLCIVGLHLEENRWYNESITALIIGLCTGVWILLMTKGRSS 74
DB 16 STSDHQSVVSINLFAVALLCIVGLHLEENRWYNESITALVIGSCTGVILLISGGKNS 75
QY 75 HLFVSEDLFFIYLLPPIIFNAGFQVKKQFFRNFTITLFGAVGTMISFFTSIAATAI 134
DB 76 HILVSEDLFFIYLLPPIIFNAGFQVKKQFFRNFTITLFGAVGTMISFFTSIAATAI 135
QY 135 FSRMNGITLDVGDFAIGAIFATSQVCTLOVLNODETPFYSLVFGGVNDATSVL 194
DB 136 FRKMNDIGLEIGDYLAIGAIFATSQVCTLOVLNODETPFYSLVFGGVNDATSVL 195
QY 195 NALQNFDLVHDAVAVLKFGLNFFYFLSSTLFGVAGLLSAYIIKKLYIGRHSTDEVA 254
DB 196 NALQNFDLSHIDTGKAMELVGNFLYLFASSTALGVAAGLLSAYIIKKLYIGRHSTDEVA 255
QY 255 LMMLMAYLSYMLAELDLGLTIVFFCGIVMSHYTHNVTSSRYTTHKAFATLSFAET 314
DB 256 IMILMAYLSYMLAELFYLSGILTVFFCGIVMSHYTHNVTSSRYTTHKAFATLSFAET 315
QY 315 FLFYVGMADALDIEKWEFASDRPGKSGISSTILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 374
DB 316 FLFYVGMADALDIEKWEFASDRPGKSGISSTILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 375
QY 375 EKITWQOQVVIWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTSTITVVLFTWVFG 434
DB 376 AKISFQOQVVIWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTSTITVVLFTWVFG 435
QY 435 MMTKPLIRILLPASGH- --PVTSESSPKSLSPHLLTSNQSGLDLESTNIVRPSLRMLL 491
DB 436 LMTKPLIRILLPASGH- --PVTSESSPKSLSPHLLTSNQSGLDLESTNIVRPSLRMLL 495
QY 492 TKPTHVHYWYKRFDDALMRPFGGRGVPFSPGSPTEQSHG 533
DB 496 STPSHTVHYWYKRFDDALMRPFGGRGVPFSPGSPTEQSHG 537
RESULT 4

AAB73253
ID AAB73253 standard; Protein; 553 AA.
XX AAB73253;
AC 14-MAY-2001 (first entry)
DT Protein regulating the pH of vacuoles.
DE Vacuole pH regulation; flower colour.
XX Nierembergia hybrida.
XX WO200114560-A1.
XX 01-MAR-2001.
XX 24-AUG-2000; 2000WO-JP05722.
XX 24-AUG-1999; 99JP-0236800.
XX (SUNR) SUNTORY LTD.
XX Iida S, Tanaka S, Inagaki Y;
PI WPI: 2001-191648/19.
DR N-PSDB; AAF75765.
XX Morning glory-originated gene encoding a protein with pH regulation
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture -
XX Example 7; Page 50-52; 68pp; Japanese.
PS The present sequence is a protein, which has vacuolar pH regulatory
XX activities. The protein enables flower colour to be controlled via
CC regulation of the vacuolar pH, colours can range from blue to red in
CC colour spectrum. The protein is useful in controlling flower colour to
CC give new breeds of colourful plants for cut flowers, particularly
CC applicable in horticulture.
XX Sequence 553 AA;
SQ Query Match 77.0%; Score 2095.5; DB 22; Length 553;
Best Local Similarity 77.8%; Pred. No. 2.3e-206;
Matches 403; Conservative 49; Mismatches 63; Indels 3; Gaps 1;
QY 15 TTSYASVVSINLFAVALLCIVGLHLEENRWYNESITALIIGLCTGVWILLMTKGRSS 74
DB 16 TTSYASVVSINLFAVALLCIVGLHLEENRWYNESITALVIGSCTGVILLISGGKNS 75
QY 75 HLFVSEDLFFIYLLPPIIFNAGFQVKKQFFRNFTITLFGAVGTMISFFTSIAATAI 134
DB 76 HILVSEDLFFIYLLPPIIFNAGFQVKKQFFRNFTITLFGAVGTMISFFTSIAATAI 135
QY 135 FSRMNGITLDVGDFAIGAIFATSQVCTLOVLNODETPFYSLVFGGVNDATSVL 194
DB 136 FRKMNDIGLEIGDYLAIGAIFATSQVCTLOVLNODETPFYSLVFGGVNDATSVL 195
QY 195 NALQNFDLVHDAVAVLKFGLNFFYFLSSTLFGVAGLLSAYIIKKLYIGRHSTDEVA 254
DB 196 NALQNFDLSHIDTGKAMELVGNFLYLFASSTALGVAAGLLSAYIIKKLYIGRHSTDEVA 255
QY 255 LMMLMAYLSYMLAELDLGLTIVFFCGIVMSHYTHNVTSSRYTTHKAFATLSFAET 314
DB 256 IMILMAYLSYMLAELFYLSGILTVFFCGIVMSHYTHNVTSSRYTTHKAFATLSFAET 315
QY 315 FLFYVGMADALDIEKWEFASDRPGKSGISSTILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 374
DB 316 FLFYVGMADALDIEKWEFASDRPGKSGISSTILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 375
QY 375 EKITWQOQVVIWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTSTITVVLFTWVFG 434

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Db 376 DKISNQVTVIWWAGLMRGAVSMALAYNOFTRGHTQLRANAIMTSTITVVLFTSVVFG 435
QY 435 MMTKPLIRILLPASGH---PVTSEPPSKSLHSPLLTSMQGSDELESTTNIVRPSSLRMLL 491
Db 436 LMTKPLILLPLPSOKHLIRMISSPMTKSFIVPLDSTQDSEADLGRHVPKPSLRMLL 495
QY 492 TKPTTVHYVYWRKFDALMRPFGRGVFPSPGSPTE 529
Db 496 STPSHTVHYVYWRKFDALMRPFGRGVFPSPGSPTE 533

RESULT 5
AAB73251
ID AAB73251 standard; Protein: 542 AA.
XX
AC AAB73251;
XX
DT 14-MAY-2001 (first entry)
XX
DE Protein regulating the pH of vacuoles.
XX
KW Vacuole pH regulation; morning glory; flower colour.
XX
OS Ipomoea nil.
XX
FN WO200114560-A1.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP05722.
XX
PR 24-AUG-1999; 99JP-0236800.
XX
PA (SUNR ) SUNTORY LTD.
XX
PI Iida S, Tanaka S, Inagaki Y;
XX
DR WPI: 2001-191648/19.
DR N-PSDB: AAF75752.
XX
PT Morning glory-originated gene encoding a protein with pH regulation
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture
XX
PS Claim 2; Page 30-33; 68pp; Japanese.
XX
CC The present sequence is a protein from Morning Glory, which has vacuolar
CC pH regulatory activities. The protein enables flower colour to be
CC controlled via regulation of the vacuolar pH, colours can range from blue
CC to red in colour spectrum. The protein is useful in controlling flower
CC colour to give new breeds of colourful plants for cut flowers,
CC particularly applicable in horticulture.
XX
SQ Sequence 542 AA;

Query Match 75.5%; Score 2055.5; DB 22; Length 542;
Best Local Similarity 76.4%; Pred. No. 2.9e-202;
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;

QY 16 TSDYASVSVSNLFFVALLCACIVLGHLLLEENRWNESTALIIIGLCTGVILLMTKGSKH 75
Db 16 TSDHASVSMNLFVALLCACIVLGHLLLEENRWNESTALIIIGLCTGVILLMTKGSKH 75
QY 76 LFVSEDLFFIYLLPPIIFNAGFVKKKOPFRNEMTITLEGAVGTMSFFTTISATIAIF 135
Db 76 LFVSEDLFFIYLLPPIIFNAGFVKKKOPFRNEMTITLEGAVGTMSFFTTISATIAIF 135
QY 136 SRMNIIGLDVGFDAIGAIFSATSDSVCTQLVINDOTPFYLSLVFGGVNDATSVLNFN 195
Db 136 KHLIDFLDFDGLAIGAIFAATSDSVCTQLVINDOTPFYLSLVFGGVNDATSVLNFN 195

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QY 196 ALQNFEDLVHDAAVVLKFLGNFFYFLSLSTFLGCVFAGLISAVIILKLYIGRHSTDEVAL 255
Db 196 AIQSEDMTSEDPKIGLHFGNLFYFLSLSTFLGCVGIGLLCAYIILKLYIGRHSTDEVAL 255
QY 256 MMLMAYLSYMLAELDLDSOILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETF 315
Db 256 MMLMSYLSYMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETF 315
QY 316 LFLYVGMADLDIEKWEFASDRPKSIGISILLGLVLIIGRAAFVPLSLSLNLTKKAPNE 375
Db 316 LFLYVGMADLDIEKWKFKVNSQGLSVAVSSILVGLILVGRAAFVPLSLSLNLTAKNSD 375
QY 376 KITRQOVVIMWAGLMRGAVSIALAYNKFTSRCHTQLHGNAMITSTITVVLFTSMVFGM 435
Db 376 KISFRQIIIMWAGLMRGAVSIALAYNKFTSTGHTSLHENAIMITSTVTVLFTSVVFG 435
QY 436 MTKPLIRILLP-----ASGHP--VTSEPPSKSLHSPLLTSMQGSDELEST--NIVRPSS 486
Db 436 MTKPLINILLPPHKQMPSGHSMITSEPPSKHFTVPLLDNQPDSESDMITGPEVARPTA 495
QY 487 LRMLLTPTHTVHYVYWRKFDALMRPFGRGVFPSPGSPTEQS 531
Db 496 LRMLLTPTHTVHYVYWRKFDALMRPFGRGVFPSPGSPTEQS 540

RESULT 6
AAY40901
ID AAY40901 standard; Protein: 538 AA.
XX
AC AAY40901;
XX
DT 18-JAN-2000 (first entry)
XX
DE Arabidopsis thaliana Na/H transporter AtNHX1.
XX
KW Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop.
XX
OS Arabidopsis thaliana.
XX
PN WO9947679-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-CA00219.
XX
PR 18-MAR-1998; 98US-0078474.
PR 15-JAN-1999; 99US-0116111.
XX
PA (BLUM/) BLUMWALD E.
PA (APSE/) APSE M.
PA (SNED/) SNEDDEN W.
PA (AHAR/) AHARON G.
XX
PI Blumwald E, Apse M, Snedden W, Aharon G;
XX
DR WPI: 1999-571840/48.
DR N-PSDB: AAZ22591.
XX
PT Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT useful in genetic engineering salt tolerance in crop plants
XX
PS Claim 36; Fig 1A; 93pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding
CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
CC and capable of increasing salt tolerance in a cell. This sequence
CC corresponds to the AtNHX1 transporter from Arabidopsis thaliana.
CC The Na/H transporter polypeptides provide a means of intracellular
CC salt management, particularly in plants. The sequences are useful for
CC producing transgenic plants that are capable of surviving in soil with
CC high salt levels that would normally inhibit growth of the crop species.

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XX 18-JAN-2000 (first entry)
 XX Arabidopsis thaliana Na/H transporter.
 XX Sodium; proton; antiporter; transporter; salt tolerance; salt management;
 KW transgenic plant; survival; soil; farming; accumulation; irrigation;
 KW crop.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN W09947679-A2.
 XX 23-SEP-1999.
 XX 18-MAR-1999; 99WO-CA00219.
 PR 18-MAR-1998; 98US-0078474.
 PR 15-JAN-1999; 99US-0116111.
 XX (BLUM/) BLUMWALD E.
 PA (APSE/) APSE M.
 PA (SNED/) SNEDDEN W.
 PA (AHAR/) AHARON G.
 XX Blumwald E, Apse M, Snedden W, Aharon G;
 PI WPI; 1999-571840/48.
 DR N-PSDB; AA22595.
 XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
 useful in genetic engineering salt tolerance in crop plants -
 Claim 50; Fig 5A-B; 93pp; English.
 The invention relates to an isolated nucleic acid molecule encoding
 a plant Na/H antiporter (PNHX) transporter polypeptide, or a fragment
 and capable of increasing salt tolerance in a cell. This sequence
 corresponds to a transporter from Arabidopsis thaliana.
 CC The Na/H transporter polypeptides provide a means of intracellular
 salt management, particularly in plants. The sequences are useful for
 producing transgenic plants that are capable of surviving in soil with
 high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 considered unproductive through salt accumulation and poor irrigation,
 e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,
 CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance.
 XX Sequence 547 AA;
 Query Match 68.1%; Score 1852.5; DB 20; Length 547;
 Best Local Similarity 72.9%; Pred. No. 2.2e-181;
 Matches 361; Conservative 55; Mismatches 76; Indels 3; Gaps 2;
 QY 3 MEVAARALGALYTTSDYASVVSINLFLVALLCIVGLHLLPENRWNSITALLIGLGTG 62
 DB 2 LDSLVKLPSL-STSDHASVVALNLFVALLCIVGLHLLPENRWNSITALLIGLGTG 60
 QY 63 VVILMTKGKSHLFFVSEDLFFIYLLPPIIFNAGFQVKKQFFNFMTIULFGAVGTMI 122
 DB 61 VTILLISKGKSHLFFVSEDLFFIYLLPPIIFNAGFQVKKQFFNFMTIULFGAVGTII 120
 QY 123 SFFITISAAIAIFRMNIGITLDVGFALGAIFSATDSVCTQLVNDQETPLLSLVFGE 182
 DB 121 SCTIISLVGTQFFKKLDIGTDFLDGDLAIGAIFAATDSVCTQLVNDQETPLLSLVFGE 180
 QY 183 GVNNDATSVLNFALQNFDLVHDAAVVLFKLGNFYFLLSSTFLGFAGLLSAYIKKL 242
 DB 181 GVNNDATSVVFNFAIQSFDLTHLNEAFAHLLGNFLFLDLSTLLGAATGLISAYIKKL 240

QY 243 YICRHSTDEVALMMLMAYLSYMLAELDLGILTVFCGIVMSHYTWHNVTESSRVTTK 302
 DB 241 YFCGRHSTDREVALMMLMAYLSYMLAELFDLSGILTVFCGIVMSHYTWHNVTESSRVTTK 300
 QY 303 HAFATLSFIAETFLFLYVGMADALDIEKWEFASDRPGKSGISILLGLVIGRAAFVFPPL 362
 DB 301 HTEFATLSFAETFLFLYVGMADALDIEKWEFASDRPGKSGISILLGLVIGRAAFVFPPL 360
 QY 363 SFLSNLTKKAPNEKITWRQOVILWAGLMRGAVSIALAYNKFTSRGHTQLHGNAMITST 422
 DB 361 SFLSNLAKKNQSEKINFNMQOVILWAGLMRGAVSIALAYNKFTSRGHTQLHGNAMITST 420
 QY 423 ITVLFSTVMFGMTKPLIRLLPASGHPVT--SEPPSKSLHSPLLTSMQSGDLESTTN 480
 DB 421 ITVLCFSTVFGMLTKPLISYLLPHQNATSMLSDDNTPKSIHPIPLLDQDSFIEPSGNHN 480
 QY 481 IVRPSSLRMLLTKPT 495
 DB 481 VPRPDSIRGFLTRPT 495
 RESULT 9
 AAU02882
 ID AAU02882 standard; Protein; 571 AA.
 XX AC AAU02882;
 XX DT 12-SEP-2001 (first entry)
 XX DE Arabidopsis thaliana AtNHX1 polypeptide.
 XX KW AtNHX1: tonoplast pyrophosphatase hydrogen ion translocating pump; AVPL;
 KW vacuolar pyrophosphatase; salt tolerance; drought tolerance; cation;
 KW freeze tolerance; 35S promoter; sodium; calcium; manganese; lead;
 KW saline soil; thale-cress.
 XX OS Arabidopsis thaliana.
 XX PN WO200133945-A1.
 XX PD 17-MAY-2001.
 XX PF 10-NOV-2000; 2000WO-US30955.
 PR 10-NOV-1999; 99US-0164808.
 PR 18-AUG-2000; 2000US-0226223.
 PR 22-AUG-2000; 2000US-0644039.
 XX (UYCO-) UNIV CONNECTICUT.
 PA (WHED) WHITEHEAD INST.
 XX PI Gaiola RA;
 XX WPI; 2001-328862/34.
 XX Transgenic plants with salt tolerance, drought and freeze resistance
 and increased yield and flower size comprise exogenous H+ genes or
 increased vacuolar pyrophosphatase expression -
 Example 1; Fig 6; 68pp; English.
 The sequence represents an Arabidopsis thaliana AtNHX1 polypeptide which
 is a tonoplast pyrophosphatase hydrogen ion (H+) translocating pump.
 CC Transgenic plants can be made by transforming plant cells with exogenous
 CC tonoplast pyrophosphatase driven H+ pump genes and an exogenous nucleic
 CC acid encoding a protein, such as AVPL, which alters expression of
 CC vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant
 CC via transformation of the cells to induce upregulation of vacuolar
 CC phosphatase expression. Drought and/or freeze tolerance may also be
 CC introduced through transformation with DNA encoding a vacuolar H+
 CC translocating pump linked to a promoter such as the 35S promoter. These
 CC processes are useful for bioremediating soil and removing cations such as
 CC sodium, calcium, manganese and lead from soil or water which can

CC support plant growth. Plants which grow in saline soil can be produced
 CC and yield and flower size of plants can be increased.

XX Sequence 571 AA;

Query Match 66.1%; Score 1799.5; DB 22; Length 571;

Best Local Similarity 68.3%; Pred. No. 6.6e-176; Mismatches 100; Indels 7; Gaps 4;

Qy 3 MEVAARALGALYTTSDYASVVSINFLVALLCACIVLGHLLLEENRWVNESITALLIGCTG 62

Db 2 LDSLVSKLPSTLSTDSHASVVALPVALLCACIVLGHLLSSNMWKNSTALLIGLGTG 60

Qy 63 VVILMHKGSKSHLSEVEDFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFCAGVTMI 122

Db 61 VTILISKGSKSHLSEVEDFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFCAGVTII 120

Qy 123 SFTTISAAIAIFSRMNTGTLDVDFLAIGAIFATSQVCTLOVLNODETPFYLSLVFGE 182

Db 121 SCTIISLCVTOFPKKLDIGTDLCDYLAICAIFAATSVCTLOVLNODETPLLSLVFCE 180

Qy 183 GVNVDATSVLNFALQNFDLVHDAAVVVKFELGNFFYLFSSSTFLGVFAGLLSAYIIKKL 242

Db 181 CVVNDATSVVVFNAIQSFDLTHLHRAAFHLLCNFLYLFLLSTLLGAATCLISAYVIKKL 240

Qy 243 YIGRSTDRVALMMLMAYLSYMLAELDLISGILTVFCGIVMSHYTHWNVTSSRVTK 302

Db 241 YFCRSTDRVALMMLMAYLSYMLARFLDLSCILTVFCGIVMSHYTHWNVTSSRITTK 300

Qy 303 HAFATLSIAETFLFYGMADLIEKWEFASDRPGSIGISILLGLVLGLRAAFVPL 362

Db 301 HTFATLSLARTFFLYVCMALDIDKWSYSDTPTGTSIAVSSILMGLVYVGRFAVPL 360

Qy 363 SFLSNLTKKAPNETWQQVYVWAGLMRGAVSTALAYNKFTSGHTOLHGNMIMTST 422

Db 361 SFLSNLAKKNSRKINFNQVYVWAGLMRGAVSTALAYNKFTSGHTOLHGNMIMTST 420

Qy 423 ITVLFSTVWFGMTKPLIRLLPASGHPVT--SEPSSPKSLRHPPLTSMOGSDLEST- 479

Db 421 ITVCLFSVVGMLTKPLISYLLPHONATTSMLSDDNTPKSIHPLLD--QDSIEPSCN 478

Qy 480 -NVRPSSRLMLLTKPTTHYVYWRKFDALMRPMFGGRGVFPVSPGSPTEQS 531

Db 479 HNVPRPDSIRGLTRPTVHYVYWRQFDDSFMRPVFCRCGRGVFPVPGSPPTERN 531

RESULT 10

AAU78424

AAU78424 standard; Protein: 556 AA.

XX AAU78424;

XX AAU78424;

DT 18-JUN-2002 (first entry)

DE Physcomitrella patens Na+/H+ antiporter PpNHX1.

XX Plant; Na+/H+ antiporter; PpNHX1; expressed sequence tag; EST;
 KW plant protectant; cytosolic; stress tolerance; plant defence activity;
 KW cancer; gall; tumour; appressorium; pathogenic stress; herbicide;
 KW insecticide; acid rain; drought tolerance; plant hormone synthesis;
 KW ultraviolet tolerance; flower development; terpene synthesis;
 KW plant organoleptic.

OS Physcomitrella patens.

XX WO200216423-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26550.

XX 25-AUG-2000; 2000US-227974P.

XX

PA (BADI) BASF PLANT SCI GMBH.

PI Da Costa Silva EO, Ishitani M;

XX WPI: 2002-292058/33.

XX New Na+/H+ antiporter nucleic acids and proteins, useful e.g. for

modulating stress tolerance in plants, or for detecting, preventing,
 conferring resistance to or treating hyperproliferative diseases, e.g.
 cancers, galls or tumours

XX Claim 1; Fig 3; 204pp; English.

XX The invention relates to novel isolated Na+/H+ antiporter coding nucleic
 acid (I) and polypeptides (II). (I) and (II) are useful in modulating the
 stress tolerance in a plant, preferably modulating a plant's tolerance
 to limited or inadequate water availability, excess salt or osmotic
 conditions, excess temperature conditions, excess metal concentration
 in soil or water, chemical stress and oxidative stress. These may also
 be used as carbon, nitrogen or carbohydrate source, in modulating plant
 defence activity, signal transduction, or metabolite transport; or as
 probes for the identification and isolation of full length cDNAs or
 genomic DNA. The polynucleotides or polypeptides are further used to
 detect, prevent, confer resistance to and/or treat hyperproliferative
 diseases such as cancers, galls, tumours, and appressorium, increase
 plant defence mechanisms against environmental or pathogenic stresses
 (e.g. viral, fungal, mycoplasma, bacterial, nematode, herbicidal,
 insecticidal, acid rain, drought, or chemical), and hormone synthesis.
 The Na+/H+ antiporter coding nucleic acids can be used in creating
 transgenic plants with desirable traits, including enhanced plant
 enhanced flower development and terpene synthesis, in expressing
 recombinant proteins to raise antibodies against polypeptides, as
 markers for tissues in which the corresponding protein is expressed, as
 chromosome markers or tags for chromosome mapping, and for genetic
 fingerprinting. The polypeptides are useful in the identification,
 prevention, and/or conferment of resistance to plant diseases,
 particularly those associated with modulating environmental stress
 responses, such as drought, freezing and salt tolerance. The polypeptides
 are further useful in modulating plant yield, development,
 differentiation, root growth, root morphology, plant colour, plant aroma,
 plant flavour, palatability of plant tissue, plant organoleptic
 properties, ability to serve as plant nutraceutical, pharmaceutical or
 phytochemical, ability to produce nutraceutical, pharmaceuticals or
 phytochemicals of either endogenous or exogenous origin. Antibodies may
 be used in diagnostic assays to detect the presence or quantity of the
 polypeptides, in affinity purification of the polypeptides from
 recombinant cell culture or natural sources, and for inhibiting allergic
 reactions in animals. The present sequence represents Physcomitrella
 patens Na+/H+ antiporter PpNHX1.

XX Sequence 556 AA;

Query Match 57.0%; Score 1550.5; DB 23; Length 556;

Best Local Similarity 60.9%; Pred. No. 2.6e-150; Mismatches 116; Indels 21; Gaps 7;

Qy 18 DYASVVSINFLVALLCACIVLGHLLLEENRWVNESITALLIGCTGVVILLMTKSSHLF 77

Db 23 DRIDVISICLVFLLCACIVLGHLLLEENRWVNESITALLIGLFTGSIVLLSSKQGGSHIL 82

Qy 78 VSEDLFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFGAVGTMTSFTTISIAAIAIFSR 137

Db 83 EFDEELFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFGVIGVIFISFGIISTGSWYFESK 142

Qy 138 MNIGTLDVGDFLAIGATFSATDSVCTLOVLNODETPPLYSLVFGEVNDATSVLNFAL 197

Db 143 FGLKNLPDIRDLAIGATFSATDSVCTLOVLNODETPPLYSLVFGEVNDATSVLNSRAV 202

Qy 198 QNEDLVHIDAADVVLKGLNFFYLFSLSTFLGVFAGLLSAYIIKKLYIGRSTDRVALMM 257

Db 203 QTYNPDNFTSLGIGGSFLYLFSSCILIASGLISAYIIKTYFGRHSTDEIAIMT 262

QY 258 LMAYLSYMLAELLDLSGILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETFLF 317
 Db 263 LMAYLSYFAELFSLGSLVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETFLF 322
 QY 318 LYVGMDALDIEKWEFASDRPKSIGISSILGLVLIGRAAFVPLSLFSLNLTKKAPNEKI 377
 Db 323 LYVGMDALDFEKWMQSFTE-ESAGLFGSLFLVLILGRAAFVPLSLNLTSTKSPDAKI 381
 QY 378 TWROQVVIWAGLMRGAVSIALAYNKKFTRSGHTQLHGNAMITSTITVVLSTWVFGHMT 437
 Db 382 NLRQMVIIWAGLMRGAVSIALAFN--QGDKARDSNQTALMVITIIIVLSTVFGTAT 438
 QY 438 KPLRLLLPASGHPVTSPPS--SPKS-----LHSPILTSMQGSDLE----STTNIVR--- 483
 Db 439 KPLISWLLPPHFRNSYSDSASLSPKASLDADFHIPLLMDTEREELEANDRSTINQILNGL 498
 QY 484 --PSSRLMLLPKPTHTVHYWYKFFDDALMRPMFGGRGV 520
 Db 499 PCPOSIGMLLTAPRSTIHHVW-KFDDSYMRPTFGGRGV 536

RESULT 11
 AAY40902
 ID AAY40902 standard; Protein: 529 AA.
 XX AC AAY40902;
 XX 18-JAN-2000 (first entry)
 DE Arabidopsis thaliana Na/H transporter AtNHX2.
 KW Sodium; proton; antiport; transporter; salt tolerance; salt management;
 KW transgenic plant; survival; soil; farming; accumulation; irrigation;
 KW crop.
 XX Arabidopsis thaliana.
 XX WO9947679-A2.
 XX 23-SEP-1999.
 XX 18-MAR-1999; 99WO-CA00219.
 XX 18-MAR-1998; 98US-0078474.
 PR 15-JAN-1999; 99US-0116111.
 XX (BLUM/) BLUMWALD E.
 PA (APSE/) APSE M.
 PA (SNED/) SNEDDEN W.
 PA (AHAR/) AHARON G.
 XX Blumwald E, Apse M, Snedden W, Aharon G;
 XX WPI; 1999-571840/48.
 DR N-PSDB; AA222592.
 XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
 PT useful in genetic engineering salt tolerance in crop plants -
 PS Claim 36; Fig 1B; 93pp; English.
 XX The invention relates to an isolated nucleic acid molecule encoding
 CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
 CC and capable of increasing salt tolerance in a cell. This sequence
 CC corresponds to the AtNHX2 transporter from Arabidopsis thaliana.
 CC The Na/H transporter polypeptides provide a means of intracellular
 CC salt management, particularly in plants. The sequences are useful for
 CC producing transgenic plants that are capable of surviving in soil with
 CC high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 CC considered unproductive through salt accumulation and poor irrigation,
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,

CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance.
 XX Sequence 529 AA;
 SQ Query Match 56.2%; Score 1529; DB 20; Length 529;
 Best Local Similarity 58.2%; Pred. No. 3.9e-148;
 Matches 297; Conservative 83; Mismatches 116; Indels 14; Gaps 5;
 QY 17 SDYASVSNIFVALLCACIVLGHLEENRWVNESITAIIGLCGVVILLMTKGSKSHL 76
 Db 15 AEHPQVIPISVFIALCLCLVGHLEENRWVNESITAILVGAASGTVILLISKGSKSHI 74
 QY 77 FVSEDLFFIYLLPIIFNAGFQVKKKOFFRNFMTITILFAGVGTMSIFFTSIAAIAIPS 136
 Db 75 LVFDEELFFIYLLPIIFNAGFQVKKKFFHNFILTFMSFGVIGVFISTVIIISFGTWLFF 134
 QY 137 RMNIGTLDVGDFLAIGALFSATDSVCTLQVLNQDETPELYSLVFGGVVNDATSIVLNFA 196
 Db 135 KLGFKGLSARDYLAIGTIFSDIVCTLIQLRQDETPLYSLVFGGVVNDATSVVLNFA 194
 QY 197 LONFDLVHIDAANVLKFLGNFFYFLPSFTFLGVFAGLLSAYIIKKLYTGRHSTDEVALM 256
 Db 195 VQIKQFESLTGWTALQVFNFLYLFSTSTLLGIGVGLITSEVLKTLYFGRHSTRELAIM 254
 QY 257 MLMAYLSYMLAELLDLSGILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETFL 316
 Db 255 VLMAYLSYMLAELFSLGILTVFFCGVLMVSHYASYNVTESSRITSRHHVAFMLSFIAETFI 314
 QY 317 FLYVGMALDIEKWEFASDRPKSIGISSILGLVLIGRAAFVPLSLFSLNLTKK--APN 374
 Db 315 FLYVGTALDFTKWTSSLSFGGTLGVSGVITALLVLLGRAAFVPLSLVLTNFMNRHTERN 374
 QY 375 EXITRQOVVIWAGLMRGAVSIALAYNKKFTRSGHTQLHGNAMITSTITVVLSTWVFG 434
 Db 375 ESITFKHQVVIWAGLMRGAVSIALAFKQFTYSGVTGLDVPVNAAMVTNTIVLFTTLVFG 434
 QY 435 MMTKPLIRLLPASGHPVT-----SEPSPK-SLHSPILTSMQGSDLESTTNIVRP--SS 486
 Db 435 FLTKPLVNYLLPQDASHNTGNRGKTEFGSPKEDATLPLLS----FDESASTNENRADS 490
 QY 487 LRMLLTPTHTVHYWYKFFDDALMRPMFGG 516
 Db 491 ISLLMEQPVVTHRYWRKFKDDTYMRPIFG 520

RESULT 12
 ABG61535
 ID ABG61535 standard; Protein: 671 AA.
 XX AC ABG61535;
 XX 27-AUG-2002 (first entry)
 DE Human transporter and ion channel, TRICH5, Incyte ID 7476938CD1.
 XX Human; transporter and ion channel; TRICH; transport disorder;
 KW neurological disorder; muscle disorder; immunological disorder; cancer;
 KW scleroderma; systemic lupus erythematosus; allergy; leukaemia;
 KW cell proliferative disorder; cervical cancer; breast cancer;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW myotonic dystrophy; catatonias; endocrine disorder; diabetes;
 KW Grave's disease; gastrointestinal disorder; Crohn's disease;
 KW renal disorder; Good pasture's syndrome; viral infection; cirrhosis;
 KW bacterial infection; fungal infection; parasitic infection;
 KW protozoal infection; helminthic infection; cardiovascular disorder;
 KW atherosclerosis; hepatic disease.
 XX Homo sapiens.
 XX WO200240541-A2.

CC encoded proteins. The invention additionally encompasses expression
 CC constructs, recombinant viruses and recombinant cells comprising the
 CC nucleic acids of the invention, recombinant production of the proteins,
 CC antibodies against the proteins, a method of identifying inhibitors of
 CC the proteins, and compositions comprising the inhibitors for
 CC administration to an animal. The nucleic acids, and the proteins they
 CC encode may be used in the prevention, treatment and diagnosis of diseases
 CC associated with flea infestations. For example, the nucleic acids may be
 CC used to produce an HMT or HNC protein according to standard recombinant
 CC DNA methodology by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
 CC and quantitate the presence of cat flea or other homologous nucleic acid
 CC sequences in samples. They may also be used to study the expression and
 CC function of the proteins and their role in metabolism. The HMT and HNC
 CC proteins may be used as antigens in the production of specific
 CC antibodies, and in assays to identify modulators (agonists and
 CC antagonists) of HMT and/or HNC protein expression and activity. The
 CC anti-HMT/HNC protein antibodies and antagonists may also be used to
 CC downregulate protein expression and activity. The antibodies may also be
 CC used as diagnostic agents for detecting the presence of flea polypeptides
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
 CC present sequence represents a cat flea HMT protein of the invention.

XX Sequence 608 AA;

Query Match 22.1%; Score 600.5; DB 21; Length 608;
 Best Local Similarity 35.1%; Pred. No. 1.4e-52;
 Matches 153; Conservative 95; Mismatches 153; Indels 35; Gaps 13;

QY 21 SVWSINLFAVALLCACIVLGHLEEN--RWVNESITALLIGLCTGVILLMTKGSSSH-- 76
 Db 81 SSMISFFVLCVALLGILLIHFMLOTGFOYLPESIVVVFVFGALIGLIINLMSSKNIANKN 140
 QY 77 -FVFSDELFFVLLPPIIFNAGFQVKKQFFRNFTITLFGAVGTMISFFTTISIAAIAIF 135
 Db 141 EEAFTPTAFVLLPPIIFESGYNLHKNFTONIGSILVFAIFGTAISAFVVG-AGVILL 199
 QY 136 SRMIG-TLVDGDFLATGAIFSDTSVCTLOVLNO--DETPELYSLVFGGVNDATSVL 193
 Db 200 GMADVYNLSFVESFAGFSLISAVDPVATVAIFHALDVPVNLNMFGEISLNDIAISIVL 259
 QY 194 FNA-LQNFDLVHDAVVKLFNGFFFLSSTFLGVFAGLLSAVIAIKKLYGRHSTDRE 252
 Db 260 TTVLESNNPLMTTAAVVGSLNFCFLMFASAGVGVFALISALLKHVDLRKIPS-LE 318
 QY 253 VALMMLMAYLSYMLAELDLGILTVFPCGIVMSHYTHWNVTSSRVTTKHAFATLSFIA 312
 Db 319 LGMMLVFTYAPYVLAEGIHLSGIMAILFCGIVMSHYTHFNLSVTQTITMQQTMRTLAFIA 378
 QY 313 ETEFLVYVGMADLDIEKWEFASDRPKSGISGILLGLVILGRAAFVFPFLSFLNLTAKA 372
 Db 379 ETCVFAIYGLMAIFSR-----HRVEPALVWSIV--ICLLIGRAANIPPLSLWLVNQFRE- 429
 QY 373 PNEKITRQOVVIMWAGLMRGAVSIALA----YKNKFRSGHTQLHGNAMITTSITVVLV 428
 Db 430 --HKITKMAFIMWFSGL-RGALSIALSLHLEFSDTEH-----VIITTLIIVLC 477
 QY 429 STWVFGMTKPLRL 444
 Db 478 TTLIFGGATMPLKFL 493

RESULT 14

ABBS9364

ID ABBS9364 standard; Protein: 649 AA.

XX AC ABBS9364;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 4884.

KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL03467.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -

XX Disclosure; SEQ ID NO 4884; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX sequences (ABL01840-ABL16175) and the encoded proteins
 XX (ABBS7737-ABBS72072).

XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIFO
 XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 649 AA;

Query Match 21.9%; Score 595.5; DB 22; Length 649;
 Best Local Similarity 35.1%; Pred. No. 5.1e-52;
 Matches 155; Conservative 88; Mismatches 155; Indels 43; Gaps 15;

QY 24 SINLFVALLCACIVLGHLEEN-----RWVNESITALLIGLCTGVILLMT--KGKSSH 75
 Db 101 SLSLFF-VICV-IMGILLIHSMLOTGFOYLPESIVVVFVFGALIGLSLVMSVGGQSGSKR 158
 QY 76 LFVFSDELFFVLLPPIIFNAGFQVKKQFFRNFTITLFGAVGTMISFFTTISIAAIAIF 135
 Db 159 EEVFSPMGFFVLLPPIIFESGYNLHKNFTONIGSILVFAIFGTTISALVIG-AGIYLL 217
 QY 136 SRMIG-TLVDGDFLATGAIFSDTSVCTLOVLNO--DETPELYSLVFGGVNDATSVL 193
 Db 218 GLGEVAFRLSFSFAGFSLISAVDPVATVAIFHALDVPVNLNMFGEISLNDIAISIVL 277
 QY 194 FNALQNFDLVHDAVVKLFNGFFFLSSTFLGVFAGLLSAVIAIKKLYGRHSTD 250
 Db 278 TASITQSANVNAEASTGEAMFSAKTCAMFFASAGVGVFALISALLKHVDLRKIPS- 336
 QY 251 REVALMMLMAYLSYMLAELDLGILTVFPCGIVMSHYTHWNVTSSRVTTKHAFATLSF 310
 Db 337 LEFAMLMFTYAPYVLAEGIHLSGIMAILFCGIVMSHYTHFNLSVTQTITMQQTMRTLAF 396
 QY 311 IAEITFLVYVGMADLDIEKWEFASDRPKSGISGILLGLV--LIGRAAFVFPFLSFLNLT 368
 Db 397 IAEITCVFAIYGLMAIFSR-----HQVELSFVIMVILCLIGRACNIFPLAFVFN- 445
 QY 369 TKKAPNEKITRQOVVIMWAGLMRGAVSIALAYKNKFRSGHTQLHGN-----IMTSTTIV 425
 Db 446 --KFRHKINNMKQFIMWFSGL-RGALSIAL-----SLHNLDSQKRVITITTLII 495

QY 426 VLFSTWVFGMMTKPLIRLLP 446
 Db 496 VLFITVLGGSTMPDLKYLKP 516

RESULT 15

ID AEEL6770 standard; Protein; 673 AA.

XX AEEL6770;

XX 09-APR-2002 (first entry)

XX Human transporter and ion channel-7 (TRICH-7) protein.

Human; transporter and ion channel-7; TRICH-7; neuroprotective; asthma; nontropic; cytosolic; cardiovascular; immunosuppressive; cardiomyopathy; antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia; Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer; amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS; Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina; cell proliferative disorder; psoriasis; cardiac disease; hypertension; bradyarrhythmia; gene expression; drug screening.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 19..38

FT /label= Transmembrane_domain

FT Domain 21..487

FT /note= "Sodium/hydrogen exchanger family domain"

FT Domain 155..173

FT /label= Transmembrane_domain

FT Domain 275..296

FT /label= Transmembrane_domain

FT Domain 457..477

FT /label= Transmembrane_domain

XX WO200192304-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US17065.

XX 26-MAY-2000; 2000US-208424P.

XX 01-JUN-2000; 2000US-209001P.

XX 08-JUN-2000; 2000US-210588P.

XX 16-JUN-2000; 2000US-212335P.

XX 22-JUN-2000; 2000US-213747P.

XX 29-JUN-2000; 2000US-215391P.

XX (INCY-) INCYTE GENOMICS INC.

XX Thornton M, Wallia NK, Yue H, Nguyen DB, Lai P, Gandhi AR;
 PI Tribouley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang Y;
 PI Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjanwala MS;
 PI Raumann BE, Lee EA, Hafalia A, Baughn MR, Green BD, Khan FA;
 PI Kearney L, Elliot VS, Seilhamer JJ, Policky JL, Borowsky ML;
 PI Burford N, Ding L, Lu DAM, Hillman JL;

XX WPI; 2002-122055/16.

XX N-PSDB; AAD27260.

XX New human transporters and ion channels (TRICH) polypeptides useful for diagnosing, treating or preventing disorders associated with aberrant expression of TRICH

XX Claim 1; Page 151-153; 210pp; English.

XX The invention relates to human transporters and ion channels (TRICH) polypeptides and their cDNA molecules. The nucleic acid and polypeptide sequences are useful in the diagnosis, treatment, and prevention of disorders associated with transport (akinesia, cystic fibrosis, Bell's

CC palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease, amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's muscular dystrophy); immunological (AIDS, Addison's disease, allergies, asthma); cell proliferative disorders (cancers, leukaemia, psoriasis); cardiac disease (angina, hypertension, or bradyarrhythmia) and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which TRICH expression may be correlated with a disease, to generate hybridization probes for mapping naturally occurring genomic sequence, and in drug screening. The present sequence is human TRICH-7 protein.

XX Sequence 673 AA;

QY Query Match 20.88; Score 565.5; DB 23; Length 673;
 Best Local Similarity 29.3%; Pred. No. 6.5e-49;
 Matches 169; Conservative 89; Mismatches 209; Indels 109; Gaps 17;

QY 23 VSINLFAVLLCACIVLGHLLLEN--RWNESITALLIIGLCTGVVILL---MTGKSSHL- 76

Db 19 VSLTFTLLTTLTTLWLFKRRVRLHEHETGLAMIVGLVILRYGTATSGRDKSL 78

QY 77 -----FVSEDLFFIYLLPPI 92

Db 79 CTQEDRAFSTLLVNVSGKFFETLTKGETSPGKINSVEQNDMLRKVTDFPEVFFNILLPPI 138

QY 93 IFNAGFOVKKQOFFRNFMTITLFGAVGTMTISFFITAAIAIFSRMTI-GTLD---VGD 147

Db 139 IFHAGYSLKKRHFNRNIGSILAYAFGLTAVSCFIIGNLMYGVVKLMIMGOLSKFYTD 198

QY 148 FLAIGAFSADTSVCTQLVNLQDETTF--LYSLVFEQGVNDATSVILFNALQNFDLVHI- 205

Db 199 CLFFGATISATDPTVVLAI FNLHADVDLYALLFGESVINDAVAILSSSIVAVQAGLN 258

QY 206 ----DAAVVLKPLGNFFYFLSSTFLGVFAGLLSAYIIK--KLIGHRSTDRVALMMLM 259

Db 259 THAFDAAAFFKSVGIFLGIFSGSFTMGAVTGVVATLVTKFKLHC---FPLLETALFFLM 315

QY 260 AYL SYMLAELLDLSGILTVFCGIVMSHYTWHNVTESSRVTTKHAFATLSFAETFLFY 319

Db 316 SWSTFLLAEACGFTGVVAVLFCGITQAHYTYNNLSVESRSRTKQLFVLFHFAENFIYSY 375

QY 320 VGMDALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVFPPLSFLSLNLTKKAPNEKITW 379

Db 376 MGLALFTQKHVS---PIFIIG---AFVAIFLGRAHHIYPLSFFNLGRR---HKIGW 425

QY 380 RQOVVIVWAGLMRGAVSTALAYNKPTRSGHTQLHGNALIMTSTTVVLFSTWVFGMMTKP 439

Db 426 NFQHMFMFSGL-RGAMAFALAIR-----DTASYARQMFTTLLIVFTVMIIGGGTTP 478

QY 440 LIRLLLPASGHPVTSE-----PSSPKSLHSPLLTSMQGSLESTNIVR 483

Db 479 MLSWLNIRVGEPEEEDONEHHWQYFRVGVDPDPPNNDSPFOVLGDG----- 529

QY 484 PSSRLMLTKPHT--VHYWYKFKFDALMRPMFGGRG 518

Db 530 PDSARGNRTKQBSAWIFRLWYSFDHNLKLPILTTHSG 565

Search completed: March 26, 2003, 18:52:28
 Job time : 77 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:51:14 ; Search time 28 Seconds
(without alignments)
562.188 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAARLALGALYTTSDYA.....GRGFVPSGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	491	18.0	832	2	US-08-677-734A-12	Sequence 12, Appl
2	491	18.0	832	4	US-09-097-053-12	Sequence 12, Appl
3	482.5	17.7	834	2	US-08-677-734A-9	Sequence 9, Appl
4	482.5	17.7	834	2	US-08-677-734A-10	Sequence 10, Appl
5	482.5	17.7	834	4	US-09-097-053-9	Sequence 9, Appl
6	482.5	17.7	834	4	US-09-097-053-10	Sequence 10, Appl
7	480.5	17.7	831	2	US-08-677-734A-11	Sequence 11, Appl
8	480.5	17.7	831	4	US-09-097-053-11	Sequence 11, Appl
9	200.5	7.4	683	4	US-09-134-001C-5576	Sequence 5576, Ap
10	130.5	4.8	635	2	US-09-014-969-11	Sequence 11, Appl
11	124.5	4.6	605	4	US-09-134-001C-4425	Sequence 4425, Ap
12	118.5	4.4	800	4	US-09-134-001C-5655	Sequence 5655, Ap
13	114	4.2	477	4	US-09-134-001C-3487	Sequence 3487, Ap
14	113	4.2	1394	4	US-09-213-053-2	Sequence 2, Appl
15	111	4.1	650	4	US-08-800-291B-4	Sequence 4, Appl
16	110	4.0	400	4	US-09-134-001C-2912	Sequence 2912, Ap
17	109.5	4.0	617	4	US-09-134-001C-4012	Sequence 4012, Ap
18	109	4.0	222	4	US-09-134-001C-4748	Sequence 4748, Ap
19	109	4.0	649	4	US-08-800-291B-5	Sequence 5, Appl
20	108	4.0	649	4	US-08-800-291B-6	Sequence 6, Appl
21	107.5	3.9	492	4	US-09-134-001C-4847	Sequence 4847, Ap
22	107	3.9	776	4	US-09-165-396-3	Sequence 3, Appl
23	104.5	3.8	518	4	US-09-134-001C-4744	Sequence 4744, Ap
24	103.5	3.8	450	4	US-09-134-001C-4858	Sequence 4858, Ap
25	103	3.8	324	4	US-09-134-001C-5525	Sequence 5525, Ap
26	103	3.8	373	4	US-09-134-001C-4029	Sequence 4029, Ap
27	103	3.8	405	4	US-09-134-001C-4999	Sequence 4999, Ap

28	101.5	3.7	434	2	US-08-529-600D-2	Sequence 2, Appl
29	101.5	3.7	434	2	US-08-973-275-4	Sequence 4, Appl
30	101.5	3.7	434	3	US-09-122-632-2	Sequence 2, Appl
31	99.5	3.7	717	4	US-08-924-629C-5	Sequence 5, Appl
32	99	3.6	525	4	US-09-351-224E-8	Sequence 8, Appl
33	97.5	3.6	530	4	US-09-134-001C-4510	Sequence 4510, Ap
34	97	3.6	2496	4	US-09-125-028-2	Sequence 2, Appl
35	96.5	3.5	299	2	US-09-097-759-3	Sequence 3, Appl
36	96.5	3.5	306	2	US-09-097-759-2	Sequence 2, Appl
37	96.5	3.5	462	2	US-08-898-976-2	Sequence 2, Appl
38	96.5	3.5	462	2	US-08-898-976-4	Sequence 2, Appl
39	96	3.5	506	4	US-09-066-047-7	Sequence 7, Appl
40	96	3.5	2958	4	US-08-894-344C-2	Sequence 2, Appl
41	95.5	3.5	438	2	US-08-677-049-9	Sequence 9, Appl
42	95.5	3.5	504	4	US-09-134-001C-5530	Sequence 5530, Ap
43	95.5	3.5	766	4	US-09-134-001C-3689	Sequence 3689, Ap
44	94	3.5	266	2	US-08-225-480-7	Sequence 7, Appl
45	94	3.5	266	2	US-09-097-759-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-677-734A-12
; Sequence 12, Application US/08677734A

; Patent No. 5871919

; GENERAL INFORMATION:

; APPLICANT: Brant, Steven R.

; APPLICANT: Yun, Chris C.H.

; APPLICANT: Donowitz, Mark

; APPLICANT: Tse, Chung-Ming

; TITLE OF INVENTION: Cloning, Tissue Distribution, and

; TITLE OF INVENTION: Functional Analysis Of The Human Na+/B+ Exchanger Isoform,

; TITLE OF INVENTION: NHE3.

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/677,734A

; FILING DATE: 10-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B.

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0043-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 832 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-677-734A-12

Query Match 18.0%; Score 491; DB 2; Length 832;

Best Local Similarity 31.7%; Pred No. 5,4e-39;

Matches 145; Conservative 88; Mismatches 172; Indels 52; Gaps 18;

Db 257 VSLGTLGVVFAFLLS--LVTR--FTKHVRRIEPPGFVFIISYLTSEMLSLAILAI 312
 QY 279 FFCGIVMSHYTHNVTTESRVTTHKATLSFIAETFLVLYVGMDALDIEKWEFASDRPG 338
 Db 313 TFCGICCOQYKANKISEQSAATVRYTKMLASSAETIIFMLGISAVNPFITWTW----- 366
 QY 339 KSIGISSILGLVLIG--RAAFVFPFLSPLNLTAKAPNEKITRQOVVIMWAGLMRGAVS 396
 Db 367 ---NTAFVLLTLVFSVYRAIGVLOTWLLNRYRMVQLEPI---DQVLSVGGI-RCAVA 419
 QY 397 ITALYNEKTRSGHQLHGNAI-----MTSTTVTVLFSTWVF-GMWTKPLIR-LLLPASGH 450
 Db 420 FALV-----VLLDGDVKKEKMLFVSTTIIIVVFTFVIFQGLTIKPLVOWLKVKRSEH 470
 QY 451 PVTSEPPSPKSLH 463
 Db 471 ---REPLNEKLH 480

RESULT 7
 US-08-677-734A-11
 ; Sequence 11, Application US/08677734A
 ; Patent No. 58/1919
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 ; TITLE OF INVENTION: NHE3.
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/677,734A
 ; FILING DATE: 10-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fordis, Jean B.
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387.0043-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 831 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-677-734A-11

Query Match 17.7%; Score 480.5; DB 2; Length 831;
 Best Local Similarity 28.6%; Pred. No. 5.7e-38;
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;
 QY 22 VVSNLFVALLCACIV-LGHLLLEENRWNNESITALIIGCTGVWILLMTKGKSSHL--FV 78
 Db 54 IIALWILVASLAKIVFHLSH--KVTSVWPESALLIVGLVGLGIV-----WAADHIASFT 106

QY 79 FSEDLEFIYLLPIIFNAGVKKKQFFRNFMTITLFGAVGTMTISFTTISIAAIAIFSRM 138
 Db 107 LPTLFFYLLPVLVDAGYFMRNLFEGNLGTLILYAVIGTWNATTCLSLYGVFLSG 166
 QY 139 NIGTLVVG--DFAIGAIFSATDSVCTQLVNLQ--DETPFLYSLVFGVGVNDATSVLNF 195
 Db 167 LMGELKIGLDFLDFGLSLIAADVPVAVLAVFEEVHVNEVLIIVFGESLINDAVTVVLYN 226
 QY 196 ALONFOLVHDAAV---VLKFLGNFVFLSSTFLGV-FAGLLSAYLIKKLYIGRHSTDR 251
 Db 227 VFSFVTLGDAVTGDCVKGIVSFFVSLGGTLGVGFAPLLS--LVTR--FTKHVRRI 282
 QY 252 EVALMLMAYLSYMLABELLDSGLITVFCGIVMSHYTHNVTTESRVTTHKAFATLSFI 311
 Db 283 EPGFVFIYSYLTSEMLSLAILAITFCGICCOQYKANKISEQSAATVRYTKMLASG 342
 QY 312 AETFLYVGMDALDIEKWEFASDRPKSGISISILLGLVLIG--RAAFVFPFLSFLSNLT 369
 Db 343 AETIIFMELGISAVDPVITW-----NTAFVLLTLVFSVYRAIGVLOTWLLNRY 393
 QY 370 KAPNEKITRQOVVIMWAGLMRGAVSIALAYNKETRSGHTQLHGNAMITSTITVVVLS 429
 Db 394 RMVQLETI---DQVMSYGGI-RCAVAYALV---VLLDEKKVKEKMLFVSTTILIVVFTT 445
 QY 430 TMVEGMMTKPLIRLLPASGHPVTSEPPSPKSLH---SPLLTSMOQSDLESTNIVRPS 485
 Db 446 VIFQGLTIKPLVOWLKVKRSE--QREPKLNEKLHGRAFDHLSAIEDISQIGHNVLRDK 503
 QY 486 SLRMLLTGKPHTVHYVYWRKFD-----DALMR 511
 Db 504 -----WSNEDRFLSKVLMR 518

RESULT 8
 US-09-097-053-11
 ; Sequence 11, Application US/09097053
 ; Patent No. 6392025
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 ; TITLE OF INVENTION: NHE3.
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/097,053
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/677,734
 ; FILING DATE: 10-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fordis, Jean B.
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387.0043-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400

100

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Best Local Similarity   20.0%; Pred. No. 7.2e-11;
Matches    86; Conservative    85; Mismatches    166; Indels     93; Gaps      1
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QY 77 FVSEDLFTYLLPPIIFNAGFOVKKKOFRFNMITLFGAVGTMISFTTISIAAIAIFS 136
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Db 53 FNFDELFMTLIAPLLFVEGVNVRSH-LRKYIKPVMMALGLVIT---TVIGVGLEI 107
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QY 137 RMNIGTLDVGDFLAICAFSATSDSVCTLOVLNQDETTP-FLYSLVFEGEVNDATSIIV--- 192
| : | | | | | | | | | : | : | : | : | : | : | : | : | : | :
Db 108 HWTWPELPIGAFAAAILCPTDAVAVOAITKGKVLPGKSMILGESULLDAAAGIISEFK 167
| : | | | | | | | | | : | : | : | : | : | : | : | : | : | :
QY 193 -----LPNALQNFDLVHIDAAVVULKFNFFYLFSSTFLGVFAGL₂LUSAVII 239
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 168 IAVGVLIITGFIFDAIOOFLIASGGAIIV-----GLTIIGMALVRFRL 210
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 240 KKLYIGRHSSTDREVALMMLMAYLSYMLAEILDLSGILTVPFCGIVMHSYTWNNVTESSRV 299
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 211 TLMRRGCIENIMFTFIQLLTPTVTYLIAELPHASGIIAAVAGLV-----HGFERDRIA 264
QY 300 TYK-----HAFNTLSFIATFTFLYVGMDDALDIKEWFASDRPGKSIGISSILLGLV 351
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 265 QTRTOLMSYNHTWSILGYVLNGVFSLGELVPEVIV-KIITEPHNLLELIVITL--- 320
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 352 LIGRAAFV-----PLSFLS-----NTKKAPNEKITWRQOVVIWAAGLM-----R 392
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 321 LVALAVYLFERFWVYVLYPYFLSYSPQKMISKNDKDVETSKPSRLYALIMTLGCVH 380
QY 393 GAVSTALAYN-KETRSGH-TOLHGNAIMTTITTVILESTMVFGMKTKPLIRLLPASGH 450
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 381 GWISIAIALTLFYLLANHETTFAYRNDDLFIASGMVIL--SLIIAQVILPLV----- 429
QY 451 PVTSEPPSPK 460
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 430 ---TPDSPK 435

RESULT 10
US-09-014-969-11
; Sequence 11, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racine, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/Ms-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 635 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-014-969-11

Query Match 4.8%; Score 130.5; DB 2; Length 635;
 Best Local Similarity 19.1%; Pred. No. 0.00041;
 Matches 118; Conservative 86; Mismatches 206; Indels 209; Gaps 25;

QY 3 MEVAARLALYTTSDYA-----SVVSINLFVALLCACIVLGHLEENRWVNESITALI 56
 DB 1 MSVGSTSAPLSPTSGTSGVSTSTFIMDYVVFVLLVLSLAIGLYHACRGWGRHTVGE 60
 QY 57 IG---LCTGVVILLMTGKS-----SHLFVSEDLFFI-----YLLPPIIFNAG 97
 DB 61 MADRKMGCLPVALLSLLATFQSAVALRVPSEIYREGTQWFLRCCYFLGLIPAHIF--- 117
 QY 98 FOVKKKQFRNPMITLFGAVGTMTSPFTISIAAIAFISRNIGTDLVGDGLAIGAI 157
 DB 118 -----IPVEYRLHL--TSAYEYLELR--FNK 139
 QY 158 TDSVCTQLVQNDPFLYSLVFGEGVNDATSIIVLFNALONFDLVHIDAADVLFKLG 217
 DB 140 TVRVC-----GVTTFIFQVIMYGVVLYAPSUAL-NAVTFGD----- 175
 QY 218 FYLFSSSTFLGVFAGLLSAYIKKIYIGRHSTDRVALMMLMAYLSYMLAEILDISGILT 277
 DB 176 --LWLSVALRIVCTVYTAGLKAIV---TDVPTLVMLFGLQALVIIVGSARKVGLGR 230
 QY 278 VFCGIVMSHYTHNVNTESSRVT-----TKHAFATLSFIATFTFLFYVGMDDALDIE 328
 DB 231 V-----WAVASQHGRISSGDFELDPDPVHRHTFTWLAFGVFMMSLYGVNQAQV 279
 QY 329 KWEEASDRPGKSGISL-----STLLGLVLIG-----RAAFVEP 361
 DB 280 R--YLSRTEKAUUSCVAVFPFQVQVSLVGLVGLVFAFYVOEYPMISQQAAPDFV 337
 QY 362 LSLFSLNLTAKAPNEKITRQVQVIVWAGLIRGAVS--IALAYNKFTSRGHTQL----- 412
 DB 338 LYFVNDLLKGLPG-----LPLGLIACLFSGSLSTISSAFNSLATVMTMEDLIRPWFPEF 390
 QY 413 -HGNAMITSTT-----VVLFTWVFGMMTKPLIRLLPASGHPV 452
 DB 391 SEARATMLSRGLAFGYGLLCLGMAYISSQMGFVLQAAISIFGMVGGPGLLGLFCIGMFPFC 450
 QY 453 TSEPSPKSLHSP-----LTSM-----QGSLESTTN--IVRPSLSRLM 490
 DB 451 ANPPGAVGLLAGLWAFWIGISIVTSMGFSMPSPSGSFSLSPTNLTATVTTMLPL 510
 QY 491 LT--KPT-----HTVHYW 502
 DB 511 TTFSEKPTGLQRYSLSYLW 529

RESULT 11
 US-09-134-001C-4425
 Sequence 4425, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4425
 LENGTH: 605
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4425

Query Match 4.6%; Score 124.5; DB 4; Length 605;
 Best Local Similarity 22.9%; Pred. No. 0.0015;
 Matches 106; Conservative 69; Mismatches 190; Indels 97; Gaps 24;

QY 22 VVSINLFVALLCACIVLGHLEENRWVNESITALIIGLCTGVVILLMTGKSSHLFVSE 81
 DB 18 MLTIVLFLAL--GIFSQWLASRIKWPISIVVMA--IVCLLVGPIFGLANKEALGPEAFSS 73
 QY 82 DLFFIYLLPPIIFNAGQVKKKQFFRNFMTITLFGAVGTMTSPFTIS-----IAAIAIF 135
 DB 74 ---IVSLAVAAIL---FEGSSNLDRE-----LKGISKAVIRIITIGAGIATILGAILH 122
 QY 136 SRMIGTLDVGDGLAIGAIFSATDSVCTQLVQNDPFLYSLVFGEGVNDATSIIVL 193
 DB 123 VTMMF-PLSIS--FVIGGLFLITGPTVIQILLKOAKVRNVDVLRWESIIIDPGLPIA 179
 QY 194 FNALQNFDELVIDAAVYLVKFLGNFFYFLSSTFLGVFAGLLSAYIIKKIYIGRHSTREV 253
 DB 180 LTAFYVVFQIFEEGIGLVVIL--FILKLLAAAILIGFCAAFLENNLI-----SQDKIP 229
 QY 254 ALMMLMAYLSYMLA-----ELDLGILVFGCGIVMSHYTHNVNTESSRVTTKHAFAT 307
 DB 230 QSLMPTQLVFLITFSGIDELISEGLLAVTIFGLMMARKKRHDLFKE---SDHFIDN 286
 QY 308 LSFTAETFLFLYVGM-----ALDIEKWERASDRPGKSGISIGSILLGLVIGRAAFVEPL 362
 DB 287 ASSILVSTFLLITSSITKDVLLNLSWL-----ILFSLVMI---VLVRPI 330
 QY 363 S-FLSNLTAKAPNEKITRQVQVIVWAGLM--RGAVSIALAYNKFTSRGHTQLHGNAM- 418
 DB 331 SVLLSTL-----GTEITKKERAVV---ALMAPRGIVVLTVA-----QFESSLFMD 372
 QY 419 -----ITS-TTIVVLFSTWVFGMMTKPLIRLLPASGHP 451
 DB 373 DKIPMAQYITPVTGVLVITVVIYGFGTPLSLKFLGVASTEP 414

RESULT 12
 US-09-134-001C-5655
 Sequence 5655, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 5655
 LENGTH: 800
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5655

Query Match 4.4%; Score 118.5; DB 4; Length 800;
 Best Local Similarity 21.3%; Pred. No. 0.0085;
 Matches 101; Conservative 71; Mismatches 173; Indels 129; Gaps 22;
 QY 57 IGLCTGVVILLMTGK-----KSSHLFVSEDL--FFIYLLPPIIFNAGFQVKKKOFFRNF 110

Db 79 LSLFGLIILSIGVGFYATQYLSHSTDNLPRFFIYLLLFMFSGMIGVIA-----NNTI 133
QY 111 TITLFGVGTMTISFFTTIS-----TAAIAIFSRMNIIGTLDVGDGLAIGAIFSATDSV 161
Db 134 LMVFEWELTSSIFULLISYWNNGESQLGAIQSPMITVFGGLALLTGFIILYIITGTNTI 193
QY 162 CTLOVNODET-----PFLYSLVFGEVGVNDATSVLNFALONFDL----- 202
Db 194 ---TDILNORNAISRHPLFIPMILMLLG-----AFTKSAQFPFHILWLPKAMAAP 240
QY 203 ---VHIDAAVVLKFLGNFFFLSTSLFVGFAGLLSAIILKKLYIGHRSTDRVALMML 258
Db 241 TPVSAYLHSAFMVK--AGIFILFRFETPL-----GLSNVYIIVTFVG-----LIT 284
QY 259 MAYLSYMLAEILDLGIL---TVFPCGVMS-----HYTWHNVTESSRVTTKHAFATLS 309
Db 285 MFLGSLTALQYDLKGLIAYSTISOLGIMTVMGLGGGYAQHTSDLSKFIYLVLFAGLF 344
QY 310 FIATFELF---LYVGMALDIEKWEFASDRPKSGISG-----ISSILLGLVLIG-- 354
Db 345 HLMHNAVFKCALFPGVGLIHE-----SGTRDIRLLNGMRKVFPKMHIVMLLAALSMAAGVP 400
QY 355 -RAAFVPLSLNLTKKAPNEKITRQOVVIMWAGLMRGAVSIALA-----YN 402
Db 401 FLNGFLSKEMFLDSLTKANELDQYGFVLTFVLISGVIASILTFYALYMIKETFNGYN 460
QY 403 --KTRSGHTOLHG-----NAIMTSTITVVLFTSTWVFGMMTKPLIRLLPAS 448
Db 461 IEKPKR---QIHEPWLFLSLPAVILMLLIPVIFPNVFGNF-----VILPAT 505

RESULT 13
US-09-134-001C-3487
; Sequence 3487, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3487
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3487

Query Match 4.2%; Score 114; DB 4; Length 477;
Best Local Similarity 20.5%; Pred. No. 0.011;
Matches 103; Conservative 84; Mismatches 189; Indels 126; Gaps 25;

QY 15 TTSYASVWSINL---FVALL-----CACIVLGHLEEN--RWVNESITA--LIIGL 59
Db 12 TTSKRNAIVTVMILSAFVSMLNOTILNTALPAIKGLNITETTAAQL---ITGFMLVNGI 68
QY 60 CTGVVILMTKGGKSHLFFVSEDLFF-----IYLLPPII--FNAGFOVKKKQ 104
Db 69 MIPLTAFMDKYSTRHYIFESMAIFLGISVAAPSPFTILMISRIIOAIGALLPLMQ 128
QY 105 FFRNFMITILFGAVGTMTISFFTTISIAAIAIFSRMNIIGTLDVGDGL-----AI 151
Db 129 ----FTVETLFPBAEQ---RCFAMGLAGVVVQSAPAIQTLTGFLVDLFSRMPFYLVSAL 181
QY 152 GAI-----FSATDSVCTLOVNODETFFLYSLVFGVGVNDATSVLNFALONFDLVI 205
Db 182 AAVAFILGFFGVENNTKTDIV-LDKISVYVS-TFGGLI-----LPAFSSVSTFGITSL 234

QY 206 DAAVVLKFLGNFFFLSTFLCVFAGLISAVYIIRK-----LYIGHRSTDRV 253
Db 235 -PVIIVTEVLGIAIIFITTRQLKHLKPLNMRVFNKVPFTLSAVSSMLVYITWVS----- 288
QY 254 ALMMLMAYLSYMLAEILDLGILTVFFCGIVMSHTVHNVTESSRVTTKHAFATL----- 308
Db 289 PALLPIYIOTGLGQSALLSGV--VVLPGAVINGLT---MVYTGKIFDKHGKVLVPGF 343
QY 309 -SFIAETFLVGVGDALDIEKWEFASDRPKSGISGILLGLVLIGRAAFVPLSFLS- 366
Db 344 ILLISMTELYSEF-----TTGPPYWFVILVYTIIRMLALGLLVMPLNTVGL 388
QY 367 NLTKAPNEKITRQOVVIMWAGLMRGAVSI---ALAYNKFTRSQHTQ-----LH 413
Db 389 NALESDDVSHGTAIINSLRIIAGAMGTAVSVTILSIVAKQYTASHSTWSKMLTOEATVH 448
QY 414 G--NAIMTSTITVVLFTSTWVF 433
Db 449 GIDVAFIETVLLIIGFTLALF 470

RESULT 14
US-09-213-053-2
; Sequence 2, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: PRT
; ORGANISM: Canine herpesvirus
US-09-213-053-2

Query Match 4.2%; Score 113; DB 4; Length 1394;
Best Local Similarity 21.6%; Pred. No. 0.067;
Matches 119; Conservative 87; Mismatches 206; Indels 140; Gaps 27;

QY 10 LGALYTTSDYASVVSINLFLVALLCACIVLGHLEENRWVNESITAILIGLCTGV----- 64
Db 454 LPCMYVT--KSLLCIGLQAGILTALIIQIL-----TESFVCSIIILATVLIIFTLSK 505
QY 65 ILLMTKCKSSHLPVSEDLF-----FYLLPPIIFNAGFQVKKQKFFRNEMTITLF 115
Db 506 ISITSFKISISICRISQIFVTIAAFCWGFDMILNPIA-----IKILI 549
QY 116 GAVGTMTISFFTTISAAIAIFSRMNI-----GTLVDGDFLAIGATFSATDSVCTLOV 166
Db 550 ----LSISFLTCTIKTHIFVLISILNGSGSHVKGSLVTLFGILGVG-----LNV 599
QY 167 LNODETPFLYSLVFGVGVNDATSVLNFALONFDLHIDAAVVLKFLGNFFYLFSSTF 226
Db 600 IK-----TEILIGPGI---ALCIILSNT--NEGLVIRDTCYVR--IGRY---KLMRTF 642
QY 227 LGVPAGILLSAYIIKKLYIGHRST--DREV-ALMMLMAYLSYMLAEILDLGILVFPFGCI 283
Db 643 TDGLHG--ASYSEDEDETSDYSEIHERKISSFQIYKYPMSIIISILGFMILTIAIWLNV 700
QY 284 VMSHYTNWNTESRVTTKHAFAT---LSFTAETFLYVGMALDIEKWEFASDRPKGS 340
Db 701 YLKNLKFH-----SPFTLVISFVGHCLAFVPEFNYKIKICSKI----- 740

QY 341 IGSSILGLVLIIGRAAFVPLSF-----LSNLTKKAPNEKITRQOVVIMWAGLMRGA- 394
Db 741 -IIICLLLEIASLVGLNFGSPILLTITTTISLVSLYIRKOT---QGVNRLAA 794
QY 395 --VSALAYNFTSRGHTQLHGNAI-----MITSTITVLFSTWVFGMTKPLIRLL 445
Db 795 TYISRALIIGYMTVGICIFYIKFTINMSFKNFYLIYVIFINLIITSASTSKPSTPTII 854
QY 446 PASGHPTVSPSSPKSLHSPLL--TSMOGSDLES--TNIVRPSSILRMLTKPHTVHYW 502
Db 855 P-----TSANESPAISIDTTTKPISTEANNLKSVSISIKPKPKLKKLLKS----- 900
QY 503 RKFDALMRPMF 514
Db 901 KCRDNVIRPVF 912

RESULT 15

US-08-800-291B-4
; Sequence 4, Application US/08800291B
; Patent No. 6153740
; GENERAL INFORMATION:
; APPLICANT: J. D. Young & C. E. Cass
; TITLE OF INVENTION: CDNA ENCODING NUCLEOSIDE TRANSPORTER
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800.291B
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/499,314
; FILING DATE: 7-JULY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07254/044W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-291B-4

Query Match 4.1%; Score 111; DB 4; Length 650;
Best Local Similarity 21.3%; Pred. No. 0.034;
Matches 98; Conservative 51; Mismatches 174; Indels 138; Gaps 19;
QY 21 SVVSNILFVALLCAC-----IVLGHLEEN-----RWVNESITA 54
Db 182 SFAGICVFVALLFACSKHCAVSMRAVSWGGLQFVLGLLVIRTERPGFIATFEMLGEQIR- 240
QY 55 LIIGLCTGVVILLMTKCKSHLVFSE----DLFFIYLLPPIIFNAGFQVKKQFFNEM 110
Db 241 -----IFLSYTRAGSS--FVFGALVKDVFQVLPPIIVFFS-----C 276
QY 111 TITLFGAVGTMISFTTISIAAIFSRMNI GTLDVGDFLAIGAIFSATDSVCTLQVLNQD 170

Db 277 VISVLVHVGLM-----QWVILKIAWLMQVMTGTTATETLSVAGNIF-----VSQT 321
QY 171 ETPFL-----YSLVPE-----GVYNDATSI VLFNALQNFDL 202
Db 322 EAPLLIRPYLADMTLSEVHVMTGGYATTIAGSLGAYISEGI--DATSLIAASVM----- 374
QY 203 VHIDAADVLFGLNFFYFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDRVALMM----- 257
Db 375 ----AAPCALALSCLVYPEVESKFRREGVKLTGYGDAQNLEAASTGAISVYKVYVANIA 430
QY 258 --LMAYLSYM-----LAELDLSGILTVPFCGIV-----MSHYTHWNYTESRVT 300
Db 431 ANLIAFLAVLDFINAAALSWLGDWVDIOGLSFQLICSYILRPVAFVLMGVANEDCPVVAELL 490
QY 301 TKHAFATLSFIATFTFLYVGMMDALDIEKWEFASDRPKSIGISILLGLVLIGRAAFVF 360
Db 491 GIKLFLN-EFVAYODLSKYKORRLAGAEW--VGDRKOWISVRAEVLTTTFTFGEANFSS 547
QY 361 PLSFLSNLTKKAPNEKITRQOVVIMWAGLMRGA-VSIALA 400
Db 548 IGIMLGLTSMVPORKSDFSQIVL---RALETGACVSLVNA 585

Search completed: March 26, 2003, 18:54:54
Job time : 34 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:53:55 ; Search time 35 seconds
(without alignments)
897.633 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MMEVAAARLALYTTSDYA.....GRGFVPRSPGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues
Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2.6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2.6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2.6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
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13: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2082	76.5	546	US-10-155-535-2	Sequence 2, Appl1
2	2023.5	74.3	538	US-09-834-998A-1	Sequence 1, Appl1
3	1931	70.9	552	US-10-155-535-4	Sequence 4, Appl1
4	561	20.6	521	US-10-155-535-6	Sequence 6, Appl1
5	545.5	20.0	446	US-10-217-096-4	Sequence 93, Appl1
6	541.5	19.9	509	US-09-800-729-93	Sequence 180, Appl1
7	541.5	19.9	526	US-09-800-729-180	Sequence 93, Appl1
8	539	19.8	645	US-10-217-096-2	Sequence 2, Appl1
9	538	19.8	669	US-09-834-998A-2	Sequence 2, Appl1
10	533	19.6	633	US-09-834-998A-3	Sequence 3, Appl1
11	485	17.6	822	US-10-217-096-6	Sequence 6, Appl1
12	478	17.6	822	US-09-824-734-3	Sequence 3, Appl1
13	314	11.5	370	US-09-800-729-215	Sequence 215, Appl1
14	292.5	10.7	339	US-09-800-729-128	Sequence 128, Appl1
15	222.5	10.7	339	US-09-800-729-129	Sequence 129, Appl1
16	285.5	10.5	1146	US-09-824-734-2	Sequence 2, Appl1
17	231.5	8.5	684	US-09-815-242-10712	Sequence 10712, A
18	210	7.7	424	US-09-824-734-4	Sequence 4, Appl1
19	192	7.1	94	US-10-217-096-5	Sequence 5, Appl1

20	184.5	6.8	686	10	US-09-815-242-5777	Sequence 5777, Ap
21	184.5	6.8	692	10	US-09-815-242-12734	Sequence 12734, A
22	133.5	5.6	516	9	US-09-738-626-5086	Sequence 5086, Ap
23	133	4.9	129	9	US-09-925-299-1210	Sequence 1210, Ap
24	133	4.9	129	9	US-09-925-299-1210	Sequence 1210, Ap
25	116.5	4.3	480	9	US-09-895-913A-92	Sequence 92, Appl1
26	110.5	4.1	450	10	US-09-815-242-5098	Sequence 385, Ap
27	109.5	4.0	296	10	US-09-815-242-5098	Sequence 5098, Ap
28	108	4.0	539	10	US-09-815-242-5139	Sequence 5139, Ap
29	105.5	3.9	461	10	US-09-815-242-12175	Sequence 12175, A
30	105.5	3.9	490	9	US-09-738-626-5881	Sequence 5881, Ap
31	105	3.9	422	10	US-09-815-242-5682	Sequence 5682, Ap
32	105	3.9	458	9	US-09-738-626-3686	Sequence 3686, Ap
33	104	3.8	444	9	US-09-738-626-6577	Sequence 6577, Ap
34	104	3.8	816	9	US-09-252-088-5	Sequence 5, Appl1
35	103.5	3.8	388	10	US-09-815-242-11458	Sequence 11458, A
36	103.5	3.8	388	10	US-09-881-752A-350	Sequence 350, Appl
37	102	3.7	494	12	US-10-033-109-6	Sequence 6, Appl1
38	99.5	3.7	717	9	US-09-883-343A-5	Sequence 5, Appl1
39	99.5	3.7	1042	10	US-09-888-615-74	Sequence 74, Appl1
40	99	3.6	371	9	US-09-759-130B-281	Sequence 281, App
41	99	3.6	525	9	US-09-882-694-8	Sequence 8, Appl1
42	99	3.6	962	9	US-09-738-626-3800	Sequence 3800, Ap
43	99	3.6	1116	9	US-09-835-976B-12	Sequence 12, Appl1
44	97	3.6	497	10	US-09-734-676-2	Sequence 2, Appl1
45	97	3.6	807	10	US-09-895-686-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-155-535-2
; Sequence, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apse, Maris
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; FILE REFERENCE: 529152000720
; CURRENT APPLICATION NUMBER: US/10/155,535
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-155-535-2

Query Match 76.5%; Score 2082; DB 9; Length 546;

Best Local Similarity 76.6%; Pred. No. 7.8e-175;

Mismatches 54; Indels 8; Gaps 2;

QY	15	TTSDYASVVSINLFWALLCACIVLGHLEENRWNESITALIGLCTGVVLLMTKGKS 74
DB	15	STSDHASVVSINLFWALLCACIVLGHLEENRWNESITALIGLCTGVVLLMTKGKS 74
QY	75	HLVFSDELFFVLLPIIFNAGFQVKKOFFNFNMTITLFGAVGTMISEFTISIAIAI 134
DB	75	HLVFSDELFFVLLPIIFNAGFQVKKOFFNFNMTITLFGAVGTMISEFTISIAIAI 134
QY	135	FSRMNIGTLDVGDPLAIGALFASATDSVCTLOVLDQNETPPLYSLVFEGGVNDATSVILF 194
DB	135	FKKLDIGTDLGDLAIGALFAATDSVCTLOVLDQNETPPLYSLVFEGGVNDATSVILF 194

Db 49 LVALMILVASLAK--IVFHLRSKVTSLVPESCLLILGLVLGGIVGAVAKAEYQL---E 103
Qy 81 EDLFEIYLLPIIFNAGQVKKOFFRNFMTITLFGAVGTMSFFFTISIA-----AIAI 134
Db 104 PGTFELFLPIVLDGSGYFNPRLFFDNLGAILTYAVVGTLNWAFITGAALWGLQOAGLV 163
Qy 135 FSRNIGTLDVGDLEATGAFSATDSVCTLOVLNQ----DETPFLYSLVFGGVVNDATSI 191
Db 164 APRVQAGLL---DFLLFGLSLISAYDPVAVLAFFVEHVNET--LFIIVFGESLLNDAVT 218
Qy 192 VLENALONF---DLVHIDAADVFLKGNFFVFLSLSTFLG--VPAGL--LSAYIIKKLYIG 245
Db 219 VLYKCNFSFVEMGSAVQATDYLGKVASLFFVSLGGAAVGLVPFALLALTRFTKRVRI- 277
Qy 246 RHSTDREVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMSHYTHWNVTESSRVTTHKAF 305
Db 278 -----IEPLLVFLAYAAAYLTAEASLSAILAVTMCGLGCKKYVEANISHKSRVTYTM 332
Qy 306 ATLSFIETFLVYGMADLDIEKWEFASDRPGKSGISILLG---LVLIGRAAFVPL 362
Db 333 KTLASCAETVIFMLLGISAYDSSKAWD-----SGLVLGTLPILFFRALGVVLQ 382
Qy 363 SFLSNLTKKAPNEKITRQOQVVIWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTST 422
Db 383 TWVLNQFLVPLDKI---DOVMSYGG--RGAVAFALV---ILLDRTKVPKDYFVATT 434
Qy 423 ITVLFSTWFMGMKTKPLIR--LLLPASGHPVTSEPPSKLSHSPLLTSMOGSDLESTNI 481
Db 435 IVWFVFTVVOGLTIKPLVKLVKVRSEH---HKPTLNQELHENTFDHI----LAAVEDV 487
Qy 482 VRPSSRLMLTKPTTHVHY---WRKED-----DALMR 511
Db 488 V-----GHHGYHWDRWBEQFDKYLQLMLR 514

RESULT 12

US-09-824-734-3
; Sequence 3, Application US/09824734
; Patent No. US20020083485A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, JIAN-KANG
; APPLICANT: SHI, HUAZHONG
; APPLICANT: ISHITANI, MANABU
; APPLICANT: STEVENSON, BECKY
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
; FILE REFERENCE: 2056444US20
; CURRENT APPLICATION NUMBER: US/09/824,734
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/194,648
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-09-824-734-3

Query Match 17.6%; Score 478; DB 10; Length 822;
Best Local Similarity 28.7%; Pred. No. 1.le-33;
Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;

Qy 18 DYASV---VSINLFVALLCACIVLGHLLLE--NRWNESITALIIGLCVGVILLTKCKS 73
Db 99 DVLHVTPEISLWILLACIKMGHVFHPTISSIVPESCLLIVGLLVGGLI---KGV 154
Qy 74 SHLFVPSDELFFYLLPPIIFNAGQVKKOFFRNFMTITLFGAVGTMSFFFTIS--IAA 131
Db 155 ETPPFLQSDVFFLFLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLNWAFELGGLIYA 214
Qy 132 IAIFSRMNTGTLDVGDLEATGAFSATDSVCTLOVLNODE--TPFLYSLVFGGVVNDATS 190

Db 215 VCLVGEQINNIGLDTLLFGSIIISAVDPVAVVAVFEEIHINELLHILVFGESLLNDAVT 274
Qy 191 IVLFNALQ---NPDLVHIDAADVFLKGNFFVFLSLSTFLGVFAGLLSYIKKLYIGRH 247
Db 275 VVLYHLFEFANVDSIGI--SDIFLGLF--SFFVVALGGVGVVGVVIAAFTSR---FTSH 329
Qy 248 STDREVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMSHYTHWNVTESSRVTTHKAFAT 307
Db 330 IRVIEPLFVFLYSYMLAEILLDLSGILTVFCGIVMSHYTHWNVTESSRVTTHKAFAT 389
Qy 308 LSFIAETFLVYGMADLDIEKWEFASDRPGKSGISILLGILVIGRAAFVPLSFLS 366
Db 390 WSSVSETLFIPLFGVSTVAGSHQWNN-----TFVISTLL--FCLIAVRLVQLVLTWFI 440
Qy 367 NLTKKAPNEKITRQOQVVIWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTSTITVV 426
Db 441 N---KFRIVKLTPKDOFIITAYGGL--RGATAFSIGY--LMDKKRHPMCD--LFTALITVI 492
Qy 427 LFTWVFMGMKTKPLIR--LLLPASGHPVTSEPPSKLSHSPLLTSMOGSDLESTNIVRPS 486
Db 493 FFTVFGQMTIRPLVDLL-----AVKKQETKRSINEEHTQFLDHLTLTGIEDIC---- 542
Qy 487 LRMLLTKPTTHVHYWYKRFDDALMR 511
Db 543 -----GHYGHHWK---DKLNR 556

RESULT 13

US-09-800-729-215
; Sequence 215, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 215
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-215

Query Match 11.5%; Score 314; DB 10; Length 370;
Best Local Similarity 29.8%; Pred. No. 9.8e-20;
Matches 88; Conservative 54; Mismatches 117; Indels 36; Gaps 10;

Qy 227 LGVFAGLLSAYIIR--KLYIGRHSTDRVALMMLMAYLSYMLAEILLDLSGLTVFCGIV 284
Db 1 MGAVTGVVTLVTKTKLHC---FPLLETLFFLMSWSTFLLAACGFTGVVAVLFCGII 57
Qy 285 MSHYTHWNVTESSRVTTHKAFATLSFIAETFLVYGMADLDIEKWEFASDRPGKSGIS 344
Db 58 QAHTYNNLSVESRSRTKQLEVLHFLAENFIFSYMGLALFTFKHVFS---PIFIIG-- 112
Qy 345 SILGLVLIGRAAFVPLSFLSNLTKKAPNEKITRQOQVVIWAGLMRGAVSIALAYNKF 404
Db 113 --AFVAIFLGRAAHYPLSPFLNLGRR---HKIGNFQHMFMFSG--LGAMAFALAIR-- 164
Qy 405 TRSGHTQLHGNAIMTSTITVVLTSTVFGVGMWTKPLIRLLLPASGHPVTSEPPSKLSH 464
Db 165 ----DTASARQMFTTLLVFTVFIIGGTTPLMSWL-----NIRVGVDQDDPPNN 216
Qy 465 PLTSMOGSDLESTNIVRPSSRLMLTKPTHT--VHYWYKRFDDALMRPMEGGRG 518
Db 217 DSFVQLQDGG-----PDSARCNRTKQESAWIFRLWYFDHNYLKPILTHSG 262

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model
Run on: March 26, 2003, 18:50:39 ; Search time 21 Seconds
(without alignments)
2449.139 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAAARLGALYTTSDYA.....GRGFVPFSPGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1698.5	62.4	457	2 T01804	Na+/H+-exchanging
2	567.5	20.8	629	2 T22848	hypothetical prote
3	564.5	20.7	703	2 T26529	hypothetical prote
4	552	20.3	569	2 T37706	probable sodium/hy
5	533	19.6	633	2 S69734	hypothetical prote
6	492	18.1	832	2 A40205	Na+/H+-exchanging
7	485	17.8	809	2 A46747	Na+/H+-exchanging
8	481	17.7	816	2 S16328	Na+/H+-exchanging
9	480.5	17.7	831	2 B40204	Na+/H+-exchanging
10	479	17.6	813	2 A46748	Na+/H+-exchanging
11	478	17.6	822	2 S30198	Na+/H+-exchanging
12	476	17.5	818	2 A48858	Na+/H+-exchanging
13	474	17.4	815	2 I57487	Na+/H+-exchanging
14	472	17.3	759	2 A46188	CAMP-activated Na+
15	463	17.0	820	2 A40204	Na+/H+-exchanging
16	460.5	16.9	698	2 A57644	Na+/H+-exchanging
17	456	16.8	717	2 C40204	Na+/H+-exchanging
18	427	15.7	478	2 T18746	Na+/H+-exchanging
19	397	14.6	375	2 B40205	Na+/H+-exchanging
20	396.5	14.6	634	2 T33528	hypothetical prote
21	395	14.5	651	2 T31869	hypothetical prote
22	394.5	14.5	602	2 H88215	protein B0495.4 [I
23	393	14.4	798	2 T23539	hypothetical prote
24	385.5	14.2	660	2 T28016	hypothetical prote
25	349.5	12.8	609	2 S30910	Na+/H+-exchanging
26	343	12.6	520	2 A42383	Na+/H+-exchanging
27	316	11.6	527	1 S75063	Na+/H+-exchanging
28	312	11.5	531	2 D96827	protein F20B17.4 [
29	290	10.7	494	1 F69355	Na+/H+ antiporter

ALIGNMENTS

RESULT 1

T01804

Na+/H+-exchanging protein 3 homolog A_TM021B04.4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Oct-1999
C:Accession: T01804
R:Dante, M.; Wamsley, P.; Gibson, A.
Submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana TM021B04.
A:Reference number: Z14440
A:Accession: T01804
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-457 <DAN>
A:Cross-references: EMBL:AF007271; NID:g2191181; PID:g2191184; GSPDB:GN00063; ATSP:A-
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP:A_TM021B04.4
A:Map position: 5
A:Introns: 55/3; 95/2; 128/1; 148/1; 163/3; 240/3; 256/2; 286/3; 320/2; 400/3; 421/3

30	279.5	10.3	527	2 AE2932	Na+/H+ antiporter
31	279.5	10.3	550	2 B98350	hypothetical prote
32	276.5	10.2	575	2 D96585	hypothetical prote
33	273	10.0	684	2 T16072	hypothetical prote
34	271	10.0	528	2 T34941	probable Na+/H+ an
35	271	10.0	581	2 G83189	probable sodium/hy
36	256	9.4	565	2 H82610	sodium/proton exch
37	254	9.3	517	2 AC2070	Na+/H+ antiporter
38	244	9.0	458	2 H75278	probable Na+/H+ an
39	240	8.8	549	2 AG0441	probable probable
40	239	8.8	682	2 AC1532	probable Na+/H+ an
41	238.5	8.8	563	2 AD1019	probable sodium/hy
42	237	8.7	682	2 AC1175	probable Na+/H+ an
43	236.5	8.7	542	2 T07032	probable integral
44	231	8.5	549	1 H65214	probable Na+/H+ ex
45	230	8.4	549	2 G91259	hypothetical prote

Query Match 62.4%; Score 1698.5; DB 2; Length 457;
Best Local Similarity 74.0%; Pred. No. 9.3e-118;
Matches 333; Conservative 45; Mismatches 51; Indels 21; Gaps 3;

Qy	3	MEVAAARLGALYTTSDYAVSVINLFVALLCACIVLGHLLLEENRWVNESITALLIGLCTG	62
Db	2	LDLSLVSKLPSSL-STSDHASVVALNLFVALLCACIVLGHLLLEENRWVNESITALLIGLCTG	60
Qy	63	VVILMTKGSKSHLFVSEDLFFIYLLPPIIFNAGFQVKKOFFRNFMTITLFGAVGTMI	122
Db	61	VILLISKGSKSHLLVFSEDLFFIYLLPPIIFNAGFQVKKOFFRNFVTIMLFGAVGTII	120
Qy	123	SFFTISIAAIFSRMNTGTLDVGDFLAIGAFSATDSVCTLOVLNQDETFFLSLVFGE	182
Db	121	SCITISLGTQFFKKLDIGTDFLDGDLAIGAFATDSVCTLOVLNQDETFFLSLVFGE	180
Qy	183	GVNDATTSIVLFNALQNFDLVHDAAVVLKFLGNFFYLFSLSTFLGV-----F	230
Db	181	GVNDATTSVVVFNALQSFDELTHLNHEAFAHLLGNLFYLFLLSTLLGAAVSPLFSSLPFL	240
Qy	231	AGLLSAYTIKKLYIG-----RHSTDRVALMMLMAYLSYMLAELDLDSGILTVFPCG	282
Db	241	TGLISAYVIKKLYFCRWPHINCHRHSTDRVALMMLMAYLSYMLAELFDLSGILTVFPCG	300
Qy	283	IWMHYTHWNTSESRVTTKHAFTLSFAETFFLYVGMADLDLEKWEFASDRPGKSG	342
Db	301	IWMHYTHWNTSESRITTKHTFATLSFAETFFLYVGMADLDLDKWRVSDTPGTGIA	360
Qy	343	ISSILLGLVLIGRAAFVFPPLSFLSNLTKKAPNEKITRWQVVIWAGLMRGAVSTALAYN	402
Db	361	VSSITLMGLVWVGRAAFVFPPLSFLSNLAKKNQSEKINFNQVVIWWSGLMRGAVSMALAYN	420

QY 403 KFTBSGHTQLHGNAIMTITVTVLSTMV 432
 Db 421 KFTBSGHTVGRNAIMTITVTVLSTMV 450

RESULT 2
 T22848

hypothetical protein F57C7.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T22848
 R:White, S.
 submitted to the EMBL Data Library, February 1996

A:Reference number: Z19625
 A:Accession: T22848
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-629 <WIL>
 A:Cross-references: EMBL:Z69646; PIDN:CAA93476.1; GSPDB:GN00028; CESP:F57C7.2
 A:Experimental source: clone F57C7
 C:Genetics:
 A:Gene: CESP:F57C7.2
 A:Map position: X
 A:Introns: 33/3; 81/1; 119/2; 155/3; 207/2; 239/1; 274/2; 304/1; 354/1; 386/3; 421/3; 457/3

Query Match 20.8%; Score 567.5; DB 2; Length 629;
 Best Local Similarity 29.7%; Pred. No. 3.6e-34;
 Matches 160; Conservative 94; Mismatches 182; Indels 103; Gaps 16;

QY 3 MEVAAARLALYTTSDYASVSVINLVALCIVLGLHLEEN--RWNESITALLIGLC 60
 Db 27 LDMAAORRASNIHRM---TIIILTVSVMLIVTAWAFKHYFRFTHESGVTLYGLL 83

QY 61 TGVVIL-----LMTKGS----- 73
 Db 84 IGVIRYFGLQLQSTQFVITKNTKIVKEPPDYLMLVKEGGSVSPHYELIEGFFAD 143

QY 74 -----SHLFVSEDLFFIYLLPPIIFNAGFOVKKKOFFRNFMTITLFGAVGTMSIF 124
 Db 144 KRKKIEQIEQKSVFSEVFNKLPPIIFNAGYSLKKRHFNRNGSILAIYFIGHTISC 203

QY 125 FVISAATAIFSRMNIIGTLVDGDFLAIGAIFSATDSVCTQLQVNL--QDETFFLYSLVFGBG 183
 Db 204 FTGCLMFVFTIFQMG--YSFKELLFFGALISATDPVTIISVENDMNVEADLFAIFGGS 262

QY 184 VYNDATSVLFLNALQNFDLVHDAVVKFLGN-----FFYFLSSTFLGVFAGLLSAYTI 239
 Db 263 ALNDAVAIVLSEVIEFNST--SSEAITLQDFGSAIAGFAGVFGSLMLGFMIGCMNAFLT 320

QY 240 KKLXIGRSTDEVALMMLMAYSLMFLDLGLTGVFCGIVMSHYTHNVTESRV 299
 Db 321 KMTLISEHAL-LESSLFLVISVFLVAFCVCLTGIVSVLFCGIAQAHYTNLSDSQS 379

QY 300 TKHAFATLSFATFLLYVGMAL--DIEKWEFASDRPKSGISGILLGLVLT--GR 355
 Db 380 NTKHFFHVMVSIMESFICYIGSVFVNNQWSP-----SFLFSLISITASR 428

QY 356 AAFVPLFLSLNLTAKAPNEKTWQOVVWAGLMRGAVSIALAYNFTSGHTQLHGN 415
 Db 429 ALFYVPLSWLLNIRRR--PKIPRYQHMLFAGL-RGAMAFALA-----GRNTSTENR 478

QY 416 AIMTITVTVLSTMVFGMMTKPLIRLLPASGHPVTSE-----PSSPKSLHSP 466
 Db 479 QMIFATTAVVIVTVLNGGLTSMWIDYLOIKHGKDAIEGQRLNENSSSPADQHSOL 537

RESULT 3
 T26529

hypothetical protein Y18D10A.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26529

R:Harris, B.
 submitted to the EMBL Data Library, December 1998

A:Reference number: Z20226
 A:Accession: T26529
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-703 <WIL>
 A:Cross-references: EMBL:AL034393; PIDN:CAA22320.1; CESP:Y18D10A.6
 A:Experimental source: clone Y18D10A
 C:Genetics:
 A:Gene: CESP:Y18D10A.6
 A:Introns: 23/3; 56/1; 103/2; 246/3; 352/3; 492/2; 578/3

Query Match 20.7%; Score 564.5; DB 2; Length 703;
 Best Local Similarity 34.2%; Pred. No. 6.8e-34;
 Matches 156; Conservative 83; Mismatches 168; Indels 49; Gaps 16;

QY 7 AARLALYTTSDYASVSVINLVALCIVLGLHLEENRWNESITALLIGLCTGVVIL 66
 Db 118 AAVGNVSEKKRSLAIFLIVMLATLVHMLIVSKIHMPESLAIVALGALIG-SIL 176

QY 67 LMTKGSLSHLVFESEDLFFIYLLPPIIFNAGFOVKKKOFFRNFMTITLFGAVGTMSIF 126
 Db 177 SYRRDWESEALSPDVFVLLPPIIFENAYNLKGYFSEFVPIITFAIFGTISAMV 236

QY 127 ISIAAIAIFSRMNIIGTLVDGDF-----LAIGAIFSATDSVCTQLQVNLQDET-FFLYSLV 180
 Db 237 IG-AGLYILGALG-----IFEFTFECFAFAMISAVDPVGTLAIFOAVVESLMLVF 291

QY 181 GEGVNDATSVL-----FNALQNFDLVHDAVVKFLGNFFLYFLSSTFLGV 229
 Db 292 GESMLNDASIVLAATAALRAKSPNSLASEI--ITSAPV-----TFTMEFFESACLV 344

QY 230 FAGLSAYIILKLYIGRSTDEVALMMLMAYSLMFLDLGLTGVFCGIVMSHY 289
 Db 345 GICLSALLFKHVDL-RKTPSLEFALLIFSIYPYGAELDLSGMAILFCGISMSQFT 403

QY 290 WHNVTESSRVTKHAFATLSFIAETFLYVGMALDIEKWEFASDRPKSGISGILLG 349
 Db 404 RHNVSPIAQITFHTPTISFVAETSTFAYIGMAFTI-KLNEFA-----PWLIFWSV-- 455

QY 350 LVLCRAAFVPLFLSLNLTAKAPNEKTWQOVVWAGLMRGAVSIALA-YNKFTRS 408
 Db 456 LCLGRACNVFLAYLVNOCRK--DVOISKNQIIMFSG-MRGAVCFALVLYMDLKD-- 510

QY 409 HTQLHGNAIMTITVTVLSTMVFGMMTKPLIRLL 444
 Db 511 ----EKKSLTLTVLTLITLFTIFLGGSLPFI 542

RESULT 4
 T37706

probable sodium/hydrogen exchanger - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: T37706
 R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1997

A:Reference number: Z21738
 A:Accession: T37706
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-569 <MUR>
 A:Cross-references: EMBL:Z97208; PIDN:CAB10103.1; GSPDB:GN00066; SPDB:SPAC15A10.06
 A:Experimental source: strain 972h-; cosmid c15A10
 C:Genetics:
 A:Gene: SPDB:SPAC15A10.06
 A:Map position: 1
 A:Introns: 11/1; 116/3; 356/3
 C:Superfamily: hypothetical protein ywg

Query Match 20.3%; Score 552; DB 2; Length 569;
 Best Local Similarity 29.4%; Pred. No. 4.4e-33;

[illegible]

DB 288 FVFIISYLSYLTSEMLSLSSILATIFCGICCCQRYVKANISEQSATIVRYITMAMLASGAET 347

DB 288 FVFIISYLSYLTSEMLSLSSILATIFCGICCCQRYVKANISEQSATIVRYITMAMLASGAET 347

```

QY 315 FLFLVCGMDALDIEKWEFASDPCKSIGTSSILLGLVLIG--RAAFVFLSFLSNLTAKA 372
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 IIFMFLGISAVDPLIWTW-----NTAFVLLTLFLFVSVERAIGVVLQTLWLNRYRMV 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 373 PNEKITRWQOVITWAGLMRGVSIAlAYNKKFTRSGHTOLHGNAl---MITSTITVLF 428
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 399 QLELI---DQVMYSYGL-RGAVAFALV-----ALDGNKVKKNLNFVSTIIIVVF 445
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 429 STWVF-GMVTKPLIR-LLLPASGHPVTSEPSPKSLH 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 446 FTWIFQGLTIKPLVQWLKVRSEH---REPKLNKLIH 479
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
A46747
Na+/H+-exchanging protein NHE-2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C:/Accession: A46747
R:rise, C.M.; Levine, S.A.; Yun, C.H.; Montrose, M.H.; Little, P.J.; Pouyssegue, J. Biol. Chem. 268, 11917-11924, 1993
A:/Title: Cloning and expression of a rabbit cDNA encoding a serum-activated
A:/Reference number: A46747; MUID:94280159; PMID:7685025
A:/Accession: A46747
A:/Status: preliminary
A:/Molecule type: nucleic acid
A:/Residues: 1-809 <TSE>
A:/Experimental source: ileal villus cells
A:/Note: sequence extracted from NCBI backbone (NCBIN:133350, NCBIPI:133351)

```

Na⁺/H⁺-exchanging protein - rabbit

N:Alternate names: Na⁺/H⁺ antiporter; Na⁺/H⁺ exchanger; pH regulatory protein

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-2000

C:Accession: S16328; S13926; S30602

R:Tse, C.M.; Ma, A.I.; Yang, V.W.; Watson, A.J.M.; Levine, S.; Montrose, M.H.; Potter EMBO J. 10, 1957-1967, 1991

A:Title: Molecular cloning and expression of a cDNA encoding the rabbit ileal villus Na⁺/H⁺ exchanger.

A:Reference number: S16328; MUID:91293086; PMID:1712287

A:Accession: S16328

A:Molecule type: mRNA

A:Residues: 1-816 <TSE>

A:Cross-references: EMBL:X59935; NID:g1642; PIDN:CAA42558.1; PID:g1643

R:Fliegel, L.; Sardet, C.; Pouyssegur, J.; Barr, A.

FEBS Lett. 279, 25-29, 1991

A:Title: Identification of the protein and cDNA of the cardiac Na⁺/H⁺ exchanger.

A:Reference number: S13926; MUID:91138752; PMID:1704856

A:Accession: S13926

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 472-816 <FLI>

A:Cross-references: EMBL:X56536; NID:g1666; PIDN:CAA39881.1; PID:g1667

R:Hildebrandt, F.; Pizzonia, J.H.; Reilly, R.F.; Reboucas, N.A.; Sardet, C.; Pouyssegur Biochim. Biophys. Acta 1129, 105-108, 1991

A:Title: Cloning, sequence, and tissue distribution of a rabbit renal Na⁺/H⁺ exchanger.

A:Reference number: S30602; MUID:92096447; PMID:1661611

A:Accession: S30602

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-241, 'A', 243-568, 'E', 570-816 <HIL>

A:Cross-references: EMBL:X61504; NID:g1653; PIDN:CAA43721.1; PID:g1654

A:Note: The authors translated the codon CTG for residue 646 as Val and GCG for residue

Qy 365 LSNLTAKAPNEKITWROQVYVWAGLMRGAVSIALAYNKKFTRSGHTOLHGNAMITSTIT 424
 Db 435 FIN---KPRIVKLPKQDFIAYGGL-RGAIAFSLGY--LLDKHFFMCD--LFLTAIT 486
 Qy 425 VVLFSTWFGMNTKPLRLILPASGHPVTSEPPSPKSLHSPILTSMOGSDLESTTNIVRP 484
 Db 487 VIFTVFOGNTIRPLVDLL-----AVKKOETKRSINEEHTQFDLHLLTGIEDIC-- 538
 Qy 485 SSLRMLTKPHTVHYVWRKFDALMR 511
 Db 539 -----GHYGHHWK---DKLNR 552

RESULT 9
 B40204
 Na+/H+-exchanging protein 3 - rat
 N:Alternate names: Na+/H+ antiporter
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
 C:Accession: B40204
 R:Orlowski, J.; Kandasamy, R.A.; Shull, G.E.
 J. Biol. Chem. 267, 9331-9339, 1992
 A:Title: Molecular cloning of putative members of the Na/H exchanger gene family. cDNA
 rally related proteins.
 A:Reference number: A40204; MUID:92250539; PMID:1577762
 A:Accession: B40204
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-831 <ORL>
 A:Cross-references: GB:M85300; NID:g205706; PIDN:AAA41702.1; PID:g205707
 C:Keywords: transmembrane protein

Query Match 17.7%; Score 480.5; DB 2; Length 831;
 Best Local Similarity 28.6%; Pred. No. 1.3e-27;
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;

Qy 22 VVSNLFVALLCACIV-LGHLEENRWVNESITALLIGLCGVVILLMTKCKSHL--FV 78
 Db 54 IIALMILVASLAKIVFHLSH--KVTSVVPESALLIVIGLVGGIV-----WAADHIASFT 106
 Qy 79 FSEDLFYLLPPIIFNAGQVKKQFFRNFTITLFGAVGTMLSFFTISIAAIAFSRM 138
 Db 107 LTPTLFFYLLPPIVDAGYENPRLFPFNLGTLTYAVIGTINNAATGLSLYGVFLSG 166
 Qy 139 NGITLDVG--DFLAIGAIFSDTCTLOVNO--DETFFLSLVFEGGVNDATSVILFN 195
 Db 167 LMGEUKIGLLDPLFGSLIAADVPVAVLAEVHVNEVLFIIIFGESSLLNDVAVVLYN 226
 Qy 196 ALQNFEDLVHIDAAV---VLKELGNFFYLLFSLSTFLGV--FAGLLSAYIIKKLYIGRHSTDR 251
 Db 227 VFESFVTLGGDAVTGDCVKGVISFFVYSLGTLGVIFAFLS--LVTR--FTKHKVRII 282
 Qy 252 EVALMMLMAYLSYMLAEILLDISGILTVFECGIVMSHYTHWNVTSRRTTKHATLSFI 311
 Db 283 EPGFVFVSYLSYLTSEMLSLAISAILAITFCGICCKQYVKANISEQSATTVRYTKMLASG 342
 Qy 312 ATEFLVYGMADALDIEKWEFASDRPGKSGISGTSLLGLVLIG--RAAFVPLSFLSNLT 369
 Db 343 AETIIFMFLGISAVDPVINTW-----NTAFVLLLVLSVYRAIGVQLVQWILNRY 393
 Qy 370 KKAPNEKITWROQVYVWAGLMRGAVSIALAYNKKFTRSGHTQLHGNAMITSTITVLF 429
 Db 394 RMVQLETI--DOVMSYGG-LRGAVAYALV---VLLDEKKVKEKLFVSTTLIVVFT 445
 Qy 430 TWVFGMNTKPLRLILPASGHPVTSEPPSPKSLH-----SPLITSMOGSDLESTTNIVRPS 485
 Db 446 VIFQGLTIKPLVQLVKVRSE--QREPKLNEKLHGRAFDHLSAIEDISGQIGHNLYRDK 503
 Qy 486 SLRMLTKPHTVHYVWRKFD-----DALMR 511
 Db 504 -----WSNFKRFLSKVLMLR 518

RESULT 10
 A46748
 Na+/H+-exchanging protein NHE-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A46748; A47449
 R:Wang, Z.; Orlowski, J.; Shull, G.E.
 J. Biol. Chem. 268, 11925-11928, 1993
 A:Title: Primary structure and functional expression of a novel gastrointestinal isof
 A:Reference number: A46748; MUID:93280160; PMID:7685026
 A:Accession: A46748
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-813 <WAN>
 A:Cross-references: GB:L11236; NID:g205318; PIDN:AAA72350.1; PID:g205319
 R:Collins, J.F.; Honda, T.; Knobel, S.; Bulus, N.M.; Conary, J.; DuBois, R.; Ghishan,
 Proc. Natl. Acad. Sci. U.S.A. 90, 3938-3942, 1993
 A:Title: Molecular cloning, sequencing, tissue distribution, and functional expressio
 A:Reference number: A47449; MUID:93248205; PMID:7683411
 A:Accession: A47449
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 117-813 <COL>
 A:Experimental source: intestine
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:130778, NCBI:P:130779)

Query Match 17.6%; Score 479; DB 2; Length 813;
 Best Local Similarity 27.3%; Pred. No. 1.6e-27;
 Matches 143; Conservative 95; Mismatches 206; Indels 80; Gaps 19;

Qy 16 TSDYASV---VSINLFVALLCACIVLGHLEENRWVNESITALLIGLCGVVILLMTKG 71
 Db 73 TLDYPHVQIPFETLWILLASLAKIGFHLKLPVTPESCILLIMVGLLGGIFGVD- 131
 Qy 72 KSHLFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFTITLFGAVGTMLSFFTISIAA 131
 Db 132 KSPD--AMKTDVFFYLLPPIVDAGYFMPTRPFENLGTIFWYAVVGTLWNSIGIGLSL 189
 Qy 132 IATFSRNIGTLDVG--DFLAIGAIFSDTCTLOV-LNODETFFLSLVFEGGVVND 188
 Db 190 FGICQIEAFGLSDITLLQNLFGSLISAVDPVAVLAEVHVNEQYLLVIFGESLLND 249
 Qy 189 TSIVLNFALONF-DLVHIDAIVLKFGLNFFYLLFSLSTFLGVFAGLSAY-----I 238
 Db 250 VTVVLYNLFKSFQCMKTIQTVDFAGIANFVVGIGVIGLIGLIGLIGLIGLIGL 309
 Qy 239 IKKLYIGRHSTDRVALMMLMAYLSYMLAEILLDISGILTVFECGIVMSHYTHWNVTESSR 298
 Db 310 IEPFLV-----FLYSYLSYTAEMFHLSGIMAITACAMTNKYVEENVSOXS 357
 Qy 299 VTTKHAFATLSFTAETFLVYVGMAL-DIEKWEFASDRPGKSGISGTSLLGLVLIGRAA 357
 Db 358 TTIKYFKMMLSSVSETLIFPMGVSTYGVKNHWNWA-----FVCFTLAFLIWRAL 408
 Qy 358 FVPELSELSNLTAKAPNEKITWROQVYVWAGLMRGAVSIALAY-----NKFTSRGHTQLH 413
 Db 409 GVEVLTVQVINWFRIP---LTFKQDFIAYGGL-RGAICFALVFLPATVFP- 457
 Qy 414 GNAMITSTITVLFSTWFGMNTKPLRLILPASGHPVTSEPPSPKSLHSPILTSMOGS 473
 Db 458 -KKFITAAIVVIFFTVILGITIRPLVEFLDVKKRSN--KKQAVSEIHCFFDHVK-T 513
 Qy 474 DLESTTNIVRPSLSRMLLTTPHTVHYVWR-----KFDALMRPM 513
 Db 514 GIEDVCG-----HWGNFWRDKFKKDDKYLRLK 542

RESULT 11
 S30198
 Na+/H+-exchanging protein - Chinese hamster
 N:Alternate names: Na+/H+ antiporter; Na+/H+ exchanger
 C:Species: Cricetus griseus (Chinese hamster)

A:Accession: A48858
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-818 <REF>
 A:Cross-references: GB:S71135; MID:g240706; PIDN:AAB20633.1; PID:g240707
 A:Experimental source: LLC-PK1 kidney cell line
 A:Note: sequence extracted from NCBI database (NCBIN:71135, NCBIPI:71136)

157487
 Na⁺/H⁺-exchanging hemolysin, amiloride-sensitive - human
 Name: Alternate names: Na⁺/H⁺ antiporter; NHE-1
 C.Species: Homo sapiens (man)
 C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Oct-1999
 A.CCAccession: 157487; A31311
 R.Flightel, L.; Dyck, J.R.; Wang, H.; Fong, C.; Haworth, R.S.
 Mol Cell. Biochem. 125, 137-143, 1993
 A.Title: Cloning and analysis of the human myocardial Na⁺/H⁺ exchanger.
 A.Reference number: 157487; MUID: 94111706; PMID: 8283968
 A.Accession: 157487
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-815 <FLI>
 A.Cross-references: GB:S68616; NID:G544775; PIDN:AAC60606.1; PID:G544776
 S.Sardet, C.; Franchi, A.; Pouyssegur, J.
 Cell 56, 271-280, 1989
 A.Title: Molecular cloning, primary structure, and expression of the human
 A.Reference number: A31311; MUID: 89106219; PMID: 2536298
 A.Accession: A31311
 A.Molecule type: mRNA

78 LTALLMKLGFLHLPRLSAVVPESCELTIVVGLVGLIKVIGEPP-----VDSQLFFTECL I

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:42:04 ; Search time 27 Seconds
(without alignments)
821.846 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAAARLGLYTTSDYA.....GRGFVPFSPGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues 112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	19.9	669	1 NAH6_HUMAN	Q92581 homo sapien
2	533	19.6	633	1 NAH2_YEAST	Q04121 saccharomyc
3	492	18.1	832	1 NAH3_RABIT	P26432 oryctolagus
4	485	17.8	809	1 NAH2_RABIT	P50482 oryctolagus
5	485	17.8	896	1 NAH5_HUMAN	Q14940 homo sapien
6	482.5	17.7	834	1 NAH3_HUMAN	P48764 homo sapien
7	481	17.7	816	1 NAH1_RABIT	P23791 oryctolagus
8	480.5	17.7	831	1 NAH3_RAT	P26433 rattus norv
9	480	17.6	812	1 NAH2_HUMAN	Q9ubyo0 homo sapien
10	480	17.6	839	1 NAH3_DIDNA	Q28362 didelphis m
11	479	17.6	813	1 NAH2_RAT	P48763 rattus norv
12	479	17.6	820	1 NAH1_MOUSE	Q61165 mus musculu
13	479	17.6	898	1 NAH5_RAT	Q920x2 rattus norv
14	478	17.6	822	1 NAH1_CRIGR	P48761 cricetulus
15	476	17.5	817	1 NAH1_BOVIN	Q28036 bos taurus
16	476	17.5	818	1 NAH1_PIG	P48762 sus scrofa
17	476	17.5	820	1 NAH1_RAT	P26431 rattus norv
18	474	17.4	815	1 NAH1_HUMAN	P19634 homo sapien
19	472	17.3	759	1 NAH6_ONCMY	Q01345 oncorynchu
20	456	16.8	717	1 NAH4_RAT	P26434 rattus norv
21	395	14.5	651	1 NAH3_CAEEL	O16452 caenorhabdi
22	390	14.3	667	1 NAH9_CAEEL	P35449 caenorhabdi
23	236.5	8.7	542	1 YMB7_MYCTU	Q50678 mycobacteri
24	231	8.5	549	1 YJCE_ECOLI	P32703 escherichia
25	186.5	6.9	578	1 YCGO_ECOLI	P76007 escherichia
26	159	5.8	808	1 NAH2_ZYGRO	O42701 zygosacchar
27	142.5	5.2	426	1 Y057_METJA	Q60362 methanococc
28	140.5	5.2	791	1 NAH1_ZYGRO	Q99173 zygosacchar
29	139.5	5.1	635	1 SL56_HUMAN	Q9y289 homo sapien
30	138.5	5.1	383	1 NAPA_ENTHR	P26235 enterococcu
31	137.5	5.1	985	1 NAH1_YEAST	Q99271 saccharomyc
32	133.5	4.9	422	1 YF21_METJA	Q58916 methanococc
33	131.5	4.8	759	1 NAH2_SCHPO	O14123 schizosacch

34	129	4.7	636	1 SL56_RABIT	Q9xt77 oryctolagus
35	128	4.7	504	1 NU5M_ORNAN	Q36459 ornithorhyn
36	125.5	4.6	558	1 YBAL_ECOLI	P39830 escherichia
37	124	4.6	410	1 Y588_BUCAL	P57648 buchnera ap
38	123	4.5	502	1 PUTP_SALTY	P10502 salmoneilla
39	120	4.4	634	1 SL56_RAT	O70247 rattus norv
40	118	4.4	502	1 PUTP_ECOLI	P07117 escherichia
41	117	4.3	430	1 YJGE_BACSU	P54487 bacillus su
42	116	4.3	492	1 YCLF_BACSU	P94408 bacillus su
43	116	4.3	554	1 NU5M_APILI	P34855 apis mellif
44	115.5	4.2	468	1 NAH_SCHPO	P36606 schizosacch
45	115	4.2	317	1 PSRC_WOLSU	P31077 wolfinella s

ALIGNMENTS

RESULT 1	NAH6_HUMAN	STANDARD;	PRT;	669 AA.
ID	NAH6_HUMAN			
AC	Q92581;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/hydrogen exchanger 6 (Na(+)/H(+) exchanger 6) (NHE-6).			
GN	SLC9A6 OR NHE6 OR KIAA0267.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98175963; PubMed=9507001;			
RA	Numata M., Petrecca K., Lake N., Orłowski J.;			
RT	"Identification of a mitochondrial Na+/H+ exchanger.";			
RL	J. Biol. Chem. 273:6951-6959(1998).			
RN	[2]			
PC	SEQUENCE OF 4-669 FROM N.A.			
RP	TISSUE=Bone marrow;			
RX	MEDLINE=97191544; PubMed=9039502;			
RA	Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,			
RA	Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by			
RT	analysis of cDNA clones from cell line KG-1 and brain.";			
RL	DNA Res. 3:321-329(1996).			
CC	-1- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS			
CC	THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME			
CC	AND CALCIUM HOMEOSTASIS.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.			
CC	-1- TISSUE SPECIFICITY: UBIQUITOUS; BUT IS MOST ABUNDANT IN			
CC	MITOCHONDRIUM-RICH TISSUES SUCH AS BRAIN, SKELETAL MUSCLE, AND			
CC	HEART.			
CC	-1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; AF030409; AAC39643.1; -			
DR	EMBL; D87743; BAA13449.1; -			
DR	Genew; HGNC:11079; SLC9A6.			
DR	MIM: 300231; -			
DR	InterPro; IPR0000676; Nah_ExchngR.			
DR	InterPro; IPR004709; Nah_exchang3.			
DR	Pfam; PF00999; Na_H_Exchange; 1.			
DR	PRINTS; PR01084; NAHEXCHNGR.			
DR	TIGRFAMs; TIGR00840; b_cpai; 1.			
DR	Transmembrane; Transport; Antiport; Sodium transport; Mitochondrion.			
KW				

FT TRANSMEM 28 48 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 142 162 POTENTIAL.
 FT TRANSMEM 179 199 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 FT TRANSMEM 340 360 POTENTIAL.
 FT TRANSMEM 382 402 POTENTIAL.
 FT TRANSMEM 404 424 POTENTIAL.
 FT TRANSMEM 447 467 POTENTIAL.
 FT TRANSMEM 483 503 POTENTIAL.
 SQ SEQUENCE 669 AA; F6416596229F2639 CRC64;

Query Match
 Best Local Similarity 19.9%; Score 541; DB 1; Length 669;
 Matches 104; Conservative 97; Mismatches 210; Indels 78; Gaps 18;

QY 1 MGMEVAARALGALYTTSDYASVVSINLFVALLCACIVLGHLEEN--RWNESITALLIG 58
 Db 53 MDEIIVSEKQAEHRQDSANLL--IFILLTLTLTWLFKRRARELHETGLAMIY 109

QY 59 LCTGVV-----ILMTKQKSH--LFFVSEDLFFIYLLPPIIFNAGFOVK 102
 Db 110 LLVGLVRYGIHVPDNNVTLSCEVOSSPTLLVTFDEPFENILLPPIIFVAGYSLKR 169

QY 103 KOFFRNFMTITLFGAVGTWISFTTISIAAIAFSRNIGTLDVGF-----LAIGAIFSA 157
 Db 170 RHFRNLGSLIAYAFUGTAISCFVIGSIMYGCVTLMKVTGOLAGDFYFDCLLFGAIVSA 229

QY 158 TDSVCTLOVNOETPP--IYSLVFGGVVNDATSIYFNALQNF-----DLVH-IDAAVVL 211
 Db 230 TDPVTVLAIFHELOVDVELYALLFGESVLDNDAVAIVLSSIVAYQPDGNSHTFDTAMP 289

QY 212 KFLGNFFYLLSTGLFVAGLLSAYIK--KLYIGRSTDRVALMMLMAYLSYMLAEL 269
 Db 290 KSGIFLGLFSGFAMGAATGVVTLVTKFTKL--REFQLLETGLFLMSWSTELLAEA 346

QY 270 LDLSGILTVFCCGIVMSHYTHNVTESSRVTTKHAFATLSFTAEFTFLYVGMALDTEK 329
 Db 347 WGTGVAVLFQGITQAHYTYNNLSTESQHRTKQFELNFIUAENFISYMGTLTFTFQN 406

QY 330 WEFASDRGKSGISILLGLVLIGRAAFVPLPSLSNLTKAPNEKITWROQVVIWAG 389
 Db 407 HVF-----NPTFVVG-----AFVAIFLGRAANIYPLSLLNLGRES---KIGSNFQHMMAFAG 456

QY 390 LMRGAVSIALAYNFTSRGHTQLHGNATMITSTIVVLFSTWVFGMTKPIRLLLPASG 449
 Db 457 L-RGAMAFALAIR-----DTATFARQMMFSTLLIVFTVWVGGGTAMLSCL----- 504

QY 450 HPVTSEPPSKLSHPLITSMQGSDLESTTNIVRPSSLRMLLTPTHTVHYVWRKFDAL 509
 Db 505 HIRGVDSQDQHLGVP-----ENERTTKASAWLFRM-----WYNFDHNY 545

QY 510 MRPFEGGRG 518
 Db 546 LKPLLTMSG 554

RESULT 2
 NAH2_YEAST ID NAH2_YEAST STANDARD; PRT; 633 AA.
 AC Q04121;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitochondrial sodium/hydrogen exchanger (Mitochondrial Na(+)/H(+) exchanger).
 GN NAH2 OR NHX1 OR YDR456W OR D9461.40.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
 Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
 Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
 Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
 Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
 Winant A., Yelton M., Bolstein D., Davis R.W.,
 Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98175963; PubMed=9507001;
 RX Numata M., Petrecca K., Lake N., Orłowski J.;
 RT Identification of a mitochondrial Na⁺/H⁺ exchanger.*;
 RL J. Biol. Chem. 273:6951-6959(1998).
 CC -!- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA⁺ AND K⁺ ACROSS
 THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLA VOLUME
 AND CALCIUM HOMEOSTASIS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -----
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 CC -----
 DR EMBL; U33007; AAB64861.1;
 DR SGD; S0002864; NHX1.
 DR InterPro; IPR000676; NaH_Exchange.
 DR InterPro; IPR004709; NaH_Exchange3.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR PRINTS; PR01084; NAHEXCHNGR.
 DR TIGRFAWS; TIGR00840; b_cpai; 1.
 KW Transmembrane; Transport; Antiport; Sodium transport; Mitochondrion.
 FT TRANSMEM 62 82 POTENTIAL.
 FT TRANSMEM 86 106 POTENTIAL.
 FT TRANSMEM 118 138 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 218 238 POTENTIAL.
 FT TRANSMEM 259 279 POTENTIAL.
 FT TRANSMEM 307 327 POTENTIAL.
 FT TRANSMEM 353 373 POTENTIAL.
 FT TRANSMEM 377 397 POTENTIAL.
 FT TRANSMEM 432 452 POTENTIAL.
 FT TRANSMEM 458 478 POTENTIAL.
 SQ SEQUENCE 633 AA; 70147 MW; 9B771ABDE41CEB0A CRC64;

Query Match 19.6%; Score 533; DB 1; Length 633;
 Best Local Similarity 26.2%; Pred. No. 1.le-27;
 Matches 153; Conservative 127; Mismatches 190; Indels 114; Gaps 20;

QY 16 TSDYASVVSINLFVALLCACIVLGHLEEN--RWNESITALLIGCTGVVLLMTCKGS 73
 Db 55 TEEMFSSWALFIMLLLSALWSSYLTQKRIRAVHETVLSIFYGMVIGLIRSPGHI 114

QY 74 SHLEVFSEDLFFIYLLPPIIFNAGFOVKKOFFRNFMTITLFGAVGTWISFTTISIAAIA 133
 Db 115 QDVTFTNSSYFVLLPPIILNSGYELNQVNFNNMLSILIFAIPGTFISAVVIGI-ILY 173

QY 134 IFSRMNIGTLDV--GDFLAIGAIFSATDSYCTLOVNOET--PFLYSLVFGGVNDATS 190
 Db 174 IWTFLGLESIDISFADAMSGATLSATDPVTLSIFWAYKVDPKLYTIIFGESLNDAS 233

QY 191 IVLFNALQNFEDLVHDAVAVLKFGLNFFYLLSTFLGVFAGLLSAYIIKKLYIGRST 250
 Db 234 IVMFETCQKPHGQPATFSSVFEGAGLFMTFSVLLIGVLIGLVALLLKTHHRRY-PQ 292

QY 251 REVALMMLMAYLSYMLAELDLGSLITVFFCGIVMSHYTHNVTESSRVTTKHAFATLSF 310

Db 293 IESCUILLIAYEYFFSNGCHMSGIVSLFCGILTKHYAYNMSRRSQITIKYFOLLAR 352
Qy 311 IAEITFLYVGMNDAL-DIEKWEFASDRPGKSGISSILLG- - - - -VLIGRAAFVPEPLS- - 363
Db 353 LSENFIFLYGLELLETEVE- - - - -LVYKPLLIIVAAISICVARWCAPVPLSQF 400
Qy 364 - - - - -FLSNLTKK- - - - -APNEKITRQOVVIMWAGLMRGAVSIALAYN- - - - -KF 404
Db 401 VNWYIRVKTIRMSGIGTGENISVPDE-IPYNYQMTFWAGL- - - - -RGAVGVALALGIQGEYKF 458
Qy 405 TRSGHTQLHGNAMITSTITVVLFTWVFGMMTKPLIBLLIPASGHPVTPSPSPK- - - - -SL 462
Db 459 T- - - - -LLATLVVVVILVFIIFGTTAGMLEVLNKTG-CITSEEDTSDDEFDI 505
Qy 463 HSP-LLTSMOGSDLE- - - - -STT- - - - - 479
Db 506 EAPRAINLLNGSIQTDGLPGYSDNNSPDISDOFAVSSKNKLPNNISTGGTGGGLNET 565
Qy 480 - - - - -NIVRPS- - - - -SLRMLTKPTHVHYWRKFDALMRPMF 514
Db 566 ENTSPNPARSSMDKRNLRDKLGTIFNSDSQWFQNFDEQVLKPVF 609
RESULT 3
ID NAH3_RABIT STANDARD; PRT; 832 AA.
AC P26432.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 3 (Na(+)/H(+)) exchanger 3) (NHE-3).
GN SLC9A3 OR NHE3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE=Ileal villus, and kidney cortex;
RX MEDLINE=92250540; PubMed=1374392;
RA Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
RT "Cloning and sequencing of a rabbit cDNA encoding an intestinal and
RT kidney-specific Na+/H+ exchanger isoform (NHE-3).";
RL J. Biol. Chem. 267:9340-9346(1992).
CC -|- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: INTESTINAL AND KIDNEY SPECIFIC. MOST ABUNDANT
CC IN KIDNEY CORTEX, FOLLOWED EQUALLY BY ILEUM AND ASCENDING COLON.
CC THEN KIDNEY MEDULLA AND JEJUNUM. IS ABSENT FROM DUODENUM AND
CC DESCENDING COLON.
CC -|- PTM: PHOSPHORYLATED (POSSIBLE).
CC -|- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -|- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M87007; AAA31420.1; -.
CC PIR: A40205; A40205.
CC InterPro: IPR000676; NaH_Exchngr.
CC InterPro: IPR004709; NaH_exchang3.
CC Pfam: PF00999; Na_H_Exchange; 1.

DR PRINTS: PRO1084; NAHEXCHNGR. 1.
DR TIGRFAMS: TIGR00840; D_cpal; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
KW Multigene family; Phosphorylation; Polymorphism.
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 11
FT TRANSMEM 12 27
FT DOMAIN 28 59
FT TRANSMEM 60 79
FT DOMAIN 80 81
FT TRANSMEM 82 101
FT DOMAIN 102 110
FT TRANSMEM 111 130
FT DOMAIN 131 134
FT TRANSMEM 135 154
FT DOMAIN 155 180
FT TRANSMEM 181 200
FT DOMAIN 201 209
FT TRANSMEM 210 229
FT DOMAIN 230 249
FT TRANSMEM 250 269
FT DOMAIN 270 298
FT TRANSMEM 299 319
FT DOMAIN 320 339
FT TRANSMEM 340 359
FT DOMAIN 360 366
FT TRANSMEM 367 385
FT DOMAIN 386 435
FT TRANSMEM 436 455
FT DOMAIN 456 832
FT CARBOHYD 325 325
FT VARIANT 144 144
SQ SEQUENCE 832 AA; 92748 MW; 8C8BB7C296CF8740 CRC64; 1
Query Match 18.1%; Score 492; DB 1; Length 832;
Best Local Similarity 31.3%; Pred. No. 6.9e-25;
Matches 143; Conservative 91; Mismatches 171; Indels 52; Gaps 18;
Qy 25 INLFVALLCACIVIGHLLEE-NRWYNESITAIILGLCTGVVILLMTKCKSHL--FVFESE 81
Db 57 IALWVLVASLAKIVFHLKSHKVTSSVVPESALLVGLVGLGIVL-----AADHIAFTLTP 111
Qy 82 DLFFIYLLPPIIFNAGVKKQKQFERNFTITLFCAGVTMISFFTTISIAAIAIFSRMNG 141
Db 112 TVFFIYLLPPIVDAGYFMPNRLFPFNSLGSILLIYAVGTVVNAATGSLXGVFLSGIMG 171
Qy 142 TLDSV--DFAITGAIFSATDSVCTLOVLNQ--DETDFLSLVFGVGVVNDATSVILFNALQ 198
Db 172 ELKIGLLDFLLFGSLIAAVDPVAVLAVFEVHVNEVLFIVFGESLLNDVAVTVLYNVFQ 231
Qy 199 NFDLVHIDAAV--VLKELGNFFYFLSSTFLG-VFAGLLSAYIIKKLYIGRHSTDREVA 254
Db 232 SEVTLGGDKVTVGDCVKGVSPFVVSGLTGLGVVFAFLLS--LVTR--FTKHVRVIEPG 287
Qy 255 LMLMAYLSYMLAEILLDLISGILTVFFCGIVMSHYTHVNVTVSSRVTTKHAFATLSFIAET 314
Db 288 FVFIISYLSYLTSEMLSSLLIATFCGICCKQYKANKISEQSAATTVRYTKMKLSAGAE 347
Qy 315 FLFLYVGMADALIEKWEFASDRPGKSGISSILLGLVLIG--RAAFVPLSFLSNLTAKA 372
Db 348 LIIFMFLGISAVDPLIWTW-----NTAFVLLTLLFVSFVRAIGVQLVQLLNRYRMV 398
Qy 373 PNEKITRQOVVIMWAGLMRGAVSIALAYNKTFRSGHTQLHGNAT- - - - -MITSTITVVLV 428
Db 399 QLELI- - - - -DOVVMSYGGGL-RGAVAFALV- - - - -ALLDGNKVKKNLNFVSTTIIIVF 445
Qy 429 STMVF-GMMTKPLIR-LLLPASGHPVTPSPSPSKSLH 463
Db 446 FTVIFGLTIKPLVQWLKVRSEH- - - - -REPKLNEKLH 479
RESULT 4
ID NAH2_RABIT STANDARD; PRT; 809 AA.

Menon A.G.;
 "Molecular cloning and physical and genetic mapping of a novel human
 Na⁺/H⁺ exchanger (NHES/SLC9A5) to chromosome 16q22.1";
 Genomics 25:615-622(1995).
 CC BY FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
 TRANSDUCTION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, TESTIS, SPLEEN, AND
 SKELETAL MUSCLE.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF111173; AAC98696.1; -.
 CC EMBL: U08607; AAA87678.1; -.
 CC Genew; HGNC:11078; SLC9A5.
 CC MIM; 600477; -.
 CC InterPro; IPR000676; NaH_Exchange.
 CC InterPro; IPR004709; NaH_Exchange3.
 CC Pfam; PF00999; Na_H_Exchange; 1.
 CC PRINTS; PR01084; NAHEXCHNGR.
 CC TIGRFAMs; TIGR00840; b_cpai; 1.
 CC Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation.
 FT TRANSMEM 46 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 104 124 POTENTIAL.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 201 221 POTENTIAL.
 FT TRANSMEM 247 267 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT TRANSMEM 332 352 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT TRANSMEM 429 449 POTENTIAL.
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 202 202 L -> V (IN REF. 2).
 FT SEQUENCE 896 AA; B9D234BFE0922269 CRC64;
 Query Match 17.8%; Score 485; DB 1; Length 896;
 Best Local Similarity 29.9%; Pred. No. 2.le-24;
 Matches 155; Conservative 93; Mismatches 190; Indels 80; Gaps 22;
 QY 22 VVSNLFVALICACIVLGLHLEE-NRWVNESITALIIGLCTGVILLMTKGKSSHLFVFS 80
 Db 49 LVALWILVASLAK--IVFSLSRVTSVLPESCILLGLGLVGLVAVAKAEYQL---E 103
 QY 81 EDLFFIYLLPPIIFNAGFOVKKQFFRNPMTITLFCAGVTMISFFTTISTA-----AIAI 134
 Db 104 PGTFEFLFPPIVLDGSGYMPERSLFFDNLGAILTVAVVGTSLWNAFTTGAALVGLQAGLV 163
 QY 135 FSRNMTGTLVDGDLAIGAIFATSVDVCTQLVNLQ---DETFFLSYLFGEVGVNDVSI 191
 Db 164 APRVQAGLL---DFLLFGSLISAVDPVAVLAVFEEVHVNET--LFIIVFGESLLNDVIV 218
 QY 192 VLFNALQNE---DLVHIDAIVLKLGNFFYFLFSSTELG-VFAGL--LSAVIIKKLYIG 245
 Db 219 VLKYVCNSFVMGSAVQATDYLVKGVSLFVSVSLGAAVGLVFAFLALTTRFTRVRI- 277

QY 246 RHSTDREVALMMLMAYLSYMLAEELDLGILTVFFCGIVMSHYTHNVNTESSRVTTKHAF 305
 Db 278 -----IEPLLVFLVLAAYLTAEMASIALAVTMCGLGCKKYVEANISHKSRRTVKYTM 332
 QY 306 ATLSFTAETFLYVGMALDIKWEFASDRPKSGISISILG----LVLIQRAAFVFL 362
 Db 333 KTLASCAETVIFMLLGISAVDSKAWD-----SGLVLTGLTILFLFRALGVVLQ 382
 QY 363 SFLSNLTKNAPNEKITRQOVVILWAGLMRGAVSIALAYNAKFTRSCHTOLHGNAMITST 422
 Db 383 TWVNOFRVLPDKI---DOVMSYGL-NGAVAFALV----ILLDTKVPKADYFVAT 434
 QY 423 ITVVFLESTWVFGMMTKPLIR-LLLPASGHPVTSEPSKLSHSLPLTSMQGSDELTNNI 481
 Db 435 IVVVFETVVOGLTIKPLVKWLVKRSEH---HKPTLNQELHEHTDHI-----LAAVEDV 487
 QY 482 VRPSSRLMLLTKPTHTVHHY---WRKFD-----DALMR 511
 Db 488 V-----GHHGYHYWRDRWEQFDKKYLSQLLMR 514
 RESULT 6
 NAH3_HUMAN STANDARD; PRT; 834 AA.
 ID NAH3_HUMAN
 AC P48764;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/hydrogen exchanger 3 (Na⁺/H⁺) exchanger 3 (NHIE-3).
 GN SUC9A3 OR NHE3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney cortex;
 RX MEDLINE=95358265; PubMed=7631746;
 RA Brant S.R., Yun C.H., Donowitz M., Tse C.-M.;
 RT "Cloning, tissue distribution, and functional analysis of the human
 Na⁺/H⁺ exchanger isoform, NHE3";
 RL Am. J. Physiol. 269:CI98-C206(1995).
 CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
 TRANSDUCTION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U28043; AAB48990.1; -.
 CC Genew; HGNC:11073; SLC9A3.
 CC MIM; 182307; -.
 CC InterPro; IPR000676; NaH_Exchange.
 CC InterPro; IPR004709; NaH_Exchange3.
 CC Pfam; PF00999; Na_H_Exchange; 1.
 CC PRINTS; PR01084; NAHEXCHNGR.
 CC TIGRFAMs; TIGR00840; b_cpai; 1.
 CC Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 13 24 A (M1) HYDROPHOBIC.

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FT DOMAIN 25 54 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 55 73 B (M2) HYDROPHOBIC.
FT DOMAIN 74 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 C (M3) (POTENTIAL).
FT DOMAIN 100 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 D (M4) (POTENTIAL).
FT DOMAIN 134 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 160 E (M5) (POTENTIAL).
FT DOMAIN 161 180 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 181 202 F (M5A) (POTENTIAL).
FT DOMAIN 203 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 232 G (M5B) (POTENTIAL).
FT DOMAIN 233 252 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 274 H (M6) (POTENTIAL).
FT DOMAIN 275 290 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 291 309 I (M7) (POTENTIAL).
FT DOMAIN 310 340 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 341 362 J (M8) (POTENTIAL).
FT DOMAIN 363 369 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 370 390 K (M9) (POTENTIAL).
FT DOMAIN 391 405 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 406 426 L, HYDROPHOBIC.
FT DOMAIN 427 435 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 436 456 M (M10) (POTENTIAL).
FT DOMAIN 457 834 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 834 AA; 92907 MW; 3E7CE33D65DF36F7 CRC64;

Query Match 17.7%; Score 482.5; DB 1; Length 834;
Best Local Similarity 31.4%; Pred. No. 2.9e-24;
Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;

QY 48 VNESITALIIGCTGVVILLMTGKSSHL--FVSEDLFFIYLLPPIIFNAGFQVKKQF 105
DB 82 VPESALLIVGLVGGIV-----WAADHIAFTLTPTVFFYLLPPVLDAGYFNPRLF 136
QY 106 FRNFMITLFGAVCTMSFFITIAATAIFSRMIGILDVG--DFAIGATFSATDSVCT 163
DB 137 FGNLGTILLVAVGVTVNAATTGSLYGVFLSGLMGDLQIGLDFLLFGSLMAAVIDPVAV 196
QY 164 LOVLNQ-DETPFLYSLVFGGVNDATSIYLFNALQNDLV--HIDAAVVLKFLGNFFY 219
DB 197 LAVPEEVHVNELFIVFGESLLDVAIVVLYNVFESFVALGDNVTVGDCVKIVSFFV 256
QY 220 LFLSSTFLG-VFAGLLSAYIIKKLYIGRSTDRVALMMLMAYLSYMLAELLDLSGILT 278
DB 257 VSLGGTLVGVVFAFLLS--LVTR--FTKHVRITIEPGVFIIISVLSYLTSEMLSAILAI 312
QY 279 FFCGIVMSHTVHNVTSSRVTTKHAFATLSFAETFLYVGMMDALDIEKWEFASDRPG 338
DB 313 TFCGICCKYVKANISQSATTVRYTVMKMLASSAETIIFMPLGISAVNPFITWV----- 366
QY 339 KSTGISILLGLVIG--RAAFVPLSFLSNLTKKAPNEKITWRQQVVIWAGLMRGAVS 396
DB 367 ---NTAPVLLTLVFSYRAIGVGVVQLTWLLNRYRMVQLEPI---DQVLSYVGL-RGAVA 419
QY 397 IALAYNKFTSGHTQLHGNAI-----MTSITIVLFSTWVF-QMVKPLIR-LLLPASGH 450
DB 420 FALV-----VLDGDKVKENLKFVSTIIIVWFVTFQGLTIKPLVQWLKVRSEH 470
QY 451 PVTSEPPSPKSLH 463
DB 471 ---REPLNLEKH 480

RESULT 7
NAHL1_RABIT
ID NAHL1_RABIT STANDARD; PRT; 816 AA.
AC P23791.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

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DE Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).
GN SLC9A1 OR NHE1
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=ileal villus;
RC MEDLINE=91293066; PubMed=1712287;
RA Tse C.-M., Ma A.I., Yang V.W., Watson A.J.M., Levine S.,
RA Montrose M.H., Potter J., Sartet C., Pouyssegur J., Donowitz M.;
RA "Molecular cloning and expression of a cDNA encoding the rabbit ileal
RA villus cell basolateral membrane Na+/H+ exchanger.";
RL EMBO J. 10:1957-1967(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Heart muscle;
RC MEDLINE=92096447; PubMed=1661611;
RA Hildebrandt F., Pizzonia J.H., Reilly R.F., Reboucas N.A.,
RA Sartet C., Pouyssegur J., Slayman C.W., Aronson P.S., Igarashi P.;
RA "Cloning, sequence, and tissue distribution of a rabbit renal Na+/H+
RA exchanger transcript.";
RL Biochim. Biophys. Acta 1129:105-108(1991).
RN [3]
RP SEQUENCE OF 472-816 FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Heart muscle;
RC MEDLINE=91138752; PubMed=1704856;
RA Fliegel L., Sartet C., Pouyssegur J., Barr A.;
RA "Identification of the protein and cDNA of the cardiac Na+/H+
RA exchanger.";
RL FEBS Lett. 279:25-29(1991).
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: KIDNEY AND INTESTINE.
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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CC -----
DR EMBL; X59935; CAA42558.1; -
DR EMBL; X61504; CAA43721.1; -
DR EMBL; X56536; CAA39881.1; -
DR PIR; S13926; S13926.
DR PIR; S16328; S16328.
DR InterPro; IPR000676; NaH_Exchange.
DR InterPro; IPR004709; NaH_exchange3.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR TIGRFAMs; TIGR00840; b_cpai; 1.
DR Transmembrane; Glycoprotein; Transport; Sodium transport;
DR Multiqene family; Phosphorylation.
FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 16 35 M1 (POTENTIAL).
FT DOMAIN 36 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 127 M2 (POTENTIAL).
FT DOMAIN 128 129 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 130 149 M3 (POTENTIAL).
FT DOMAIN 150 154 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 155 174 M4 (POTENTIAL).
FT DOMAIN 175 191 CYTOPLASMIC (POTENTIAL).

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Query Match      17.7%; Score 480.5; DB 1; Length 831;
Best Local Similarity 28.6%; Pred. No. 3.8e-24;
Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;

QY 22 VVINLFVALLCACIV-LGHLLENRWVNESITALIIGLCTGVVILLMTKGKSSHL--FV 78
Db 54 IIALWILVASLAKIVFHLSH--KVTSVPESSALLVLGLVGIIV-----WAADHIAST 106
QY 79 FSEDLFFIYLLPIINAGQVKKKQFFRNFMTITLFGAVGTWMSFPTISIAAIAIFSRM 138
Db 107 LPTLFFYLLPIIVLDAGYFNPRLFFGNLGTILLYAVIGTILWNAATTGLSLUGVFLSG 166
QY 139 NIGTLDVG--DFAIGAIFSDSVCTQLVINO--DETPFLYSLVFGGVVNDATSVLFN 195
Db 167 LMGEKIGLGLDFLLFGLSLIAADVPVAVLAVFEVHVNEVLFITVFGESLLNDVTVVLYN 226
QY 196 ALQNFOLVHIDAIV---VLKFLGNFFYFLSFTFLGV-FAGLLSAVLIKKLYIGRHSTDR 251
Db 227 VFESFVTLGGDAVTGDCVKGVISFPVSLGGTGLGVIFAFLS--LVTR--FTKHVRIL 282
QY 252 EVALMMLMAYLSYMLAEFLDLGSLTVFFCGIVMSHYTWHNVTVESRVTTKHAFATLSFI 311
Db 283 EPGFVFVISYLSYLTSEMLISAILAITFCGICQKQYVKANISEQSATTVRVTMKNLAGS 342
QY 312 AETFLFYVGMADLDLEKWEFASDRPKSIGISILLGLVLIG--RAAFVPLSLFSLNLT 369
Db 343 AETIFMFLGISAVDPVITW-----NTAFVLLTLFVSVRAIGVLOTWILNRY 393
QY 370 KAPNEKITWROOVVIMWAGLMRGAVSIALAYNKETRSHTQLHGNAIMITTITVTLFVS 429
Db 394 RMVQLETI---DOQVMSYGLL-RGAVAYALV---VLLDEKKVKKEKLPVSTLIVVFT 445
QY 430 TWVFGMTKPLRLILPASGHPVTSEPSPKSLH----SPLTSMQGSDELTNNIVRPS 485
Db 446 VIFQGLTTPKPLVQWLKVRSE--QREPKLNEKLHGRAFDHILSAITEDISGQIGHYLRDK 503
QY 486 SLRMLLTPTHTVHYWYRKFD-----DALMR 511
Db 504 -----WSNFDKRLSKVLMLR 518

RESULT 9
NAH2_HUMAN
ID NAH2_HUMAN STANDARD; PRT; 812 AA.
AC Q9UB0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2).
GN SLC9A2 OR NHE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=99375108; PubMed=10444453;
RA Malakooti J., Dahdal R.Y., Schmidt L., Layden T.J., Dudeja P.K.,
RA Ramaswamy K.;
RT "Molecular cloning, tissue distribution, and functional expression of
RT the human Na(+)/H(+) exchanger NHE2."
RL Am. J. Physiol. 277:G383-G390(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hou S., Wohldmann P.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
CC COLONIC SODIUM ABSORPTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND
CC KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL
CC INTESTINE.
CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF073299; AAC1635.1; -
CC EMBL: AC007239; AAF19248.1; -
CC Genew; HGNC:11072; SLC9A2.
CC MIM: 600530; -
CC InterPro: IPR000676; NaH_Exchng.
CC InterPro: IPR004709; NaH_exchang3.
CC Pfam: PF00999; Na_H_Exchange; 1.
CC PRINTS: PRO1084; NAHEXCHNGR.
CC TIGRFAMs: TIGR00840; b_cpai; 1.
CC Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
CC Multigene family; Phosphorylation.
CC DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 14 33 A (M1) HYDROPHOBIC.
CC DOMAIN 34 79 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 101 106 B (M2) HYDROPHOBIC.
CC DOMAIN 107 127 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 128 138 C (M3) (POTENTIAL).
CC DOMAIN 139 159 D (M4) (POTENTIAL).
CC DOMAIN 160 168 E (M5) (POTENTIAL).
CC DOMAIN 169 189 F (M5A) (POTENTIAL).
CC DOMAIN 190 208 G (M5B) (POTENTIAL).
CC DOMAIN 209 229 H (M6) (POTENTIAL).
CC DOMAIN 230 236 I (M7) (POTENTIAL).
CC DOMAIN 237 257 J (M8) (POTENTIAL).
CC DOMAIN 258 277 K (M9) (POTENTIAL).
CC DOMAIN 278 298 L, HYDROPHOBIC.
CC DOMAIN 299 307 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 308 328 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 361 381 J (M8) (POTENTIAL).
CC DOMAIN 382 391 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 392 412 K (M9) (POTENTIAL).
CC DOMAIN 413 429 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 430 450 L, HYDROPHOBIC.
CC DOMAIN 451 458 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 459 479 M13 (POTENTIAL).
CC DOMAIN 480 812 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 350 350 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 812 AA; 91519 MW; 17EE17DC3830D0A CRC64;
Query Match      17.6%; Score 480; DB 1; Length 812;
Best Local Similarity 27.3%; Pred. No. 4e-24;
Matches 143; Conservative 98; Mismatches 203; Indels 80; Gaps 19;

QY 16 TSDYASV---VSNLFVALLCACIVGLHLEE-NRWVNESITALIIGLCTGVVILLMTKG 71
Db 72 TLDYPHVQIPFEITLWILLASLAKIGFHYHKLPTIVPESCLIMVGLLGGIIFGVDE- 130
QY 72 KSHLFESEDLFFTYLLPPIIFNAGFOVKKQFFRNFMTITLFGAVTMTISFFPTISIAA 131
Db 131 KSPF--AMKTDVFFYLLPPIIVLDAGYFNPRLFFGNLGTILLYAVIGTILWNAATTGL 188
QY 132 IATFSRNIGTLDVG--DFAIGAIFSDSVCTQLVINO--DETPFLYSLVFGGVVNDATSV 188
Db 189 FGICQIEAFGLSDITLLQNLFLGSLISAVDPVAVLAVFENIHVNEQLYILVFGESLLNDA 248

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC TISSUE=Stomach;
 RX MEDLINE=93280160; PubMed=7685026;
 RA Wang Z., Orłowski J., Shull G.E.;
 RT "Primary structure and functional expression of a novel
 RL gastrointestinal isoform of the rat Na/H exchanger.";
 RN J. Biol. Chem. 268:11925-11928(1993).
 [2]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC STRAIN=Sprague-Dawley; TISSUE=Small intestine;
 RX MEDLINE=93248205; PubMed=7683411;
 RA Collins J.F., Honda T., Knobel S., Bulus N.M., Conary J.,
 RT "Molecular cloning, sequencing, tissue distribution, and functional
 RL expression of a Na⁺/H⁺ exchanger (NHE-2).";
 RN Proc. Natl. Acad. Sci. U.S.A. 90:3938-3942(1993).
 [3]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE=Liver;
 RX MEDLINE=96129297; PubMed=8595899;
 RA Ghishan F.K., Knobel S.M., Summar M.;
 RT "Molecular cloning, sequencing, chromosomal localization, and tissue
 RL distribution of the human Na⁺/H⁺ exchanger (SLC9A2).";
 RN Genomics 30:25-30(1995).
 CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
 CC COLONIC SODIUM ABSORPTION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: PROMINANTLY IN SMALL INTESTINE, COLON, AND
 CC STOMACH, WITH MUCH LOWER LEVELS IN SKELETAL MUSCLE, KIDNEY, BRAIN,
 CC TESTIS, UTERUS, HEART, AND LUNG.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -!- CAUTION: REF.3 SEQUENCE WAS ORIGINALLY THOUGHT TO ORIGINATE FROM
 CC HUMAN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L11236; AAA72350.1; -;
 DR EMBL; L11004; AAA75406.1; -;
 DR EMBL; S81591; AAB36180.1; -;
 DR InterPro; IPR000676; NaH_Exchngr.
 DR InterPro; IPR004709; NaH_exchngr.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR PRINTS; PR01084; NAHEXCHNGR.
 DR TIGRFAMs; TIGR00840; b_cpai; 1.
 DR Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation; Alternative splicing.
 KX -----
 FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 14 34 A (M1) HYDROPHOBIC.
 FT DOMAIN 35 80 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 81 101 B (M2) HYDROPHOBIC.
 FT DOMAIN 102 107 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 108 128 C (M3) (POTENTIAL).
 FT DOMAIN 129 139 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 140 160 D (M4) (POTENTIAL).
 FT DOMAIN 161 169 CYTOPLASMIC (POTENTIAL).

TRANSMEM 170 190 E (M5) (POTENTIAL).
 FT DOMAIN 191 209 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 210 230 F (M5A) (POTENTIAL).
 FT DOMAIN 231 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 258 G (M5B) (POTENTIAL).
 FT DOMAIN 259 278 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 279 299 H (M6) (POTENTIAL).
 FT DOMAIN 300 308 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 309 329 I (M7) (POTENTIAL).
 FT DOMAIN 330 361 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 362 382 J (M8) (POTENTIAL).
 FT DOMAIN 383 392 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 393 413 K (M9) (POTENTIAL).
 FT DOMAIN 414 430 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 431 451 L, HYDROPHOBIC.
 FT TRANSMEM 452 459 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 460 480 M13 (POTENTIAL).
 FT DOMAIN 481 813 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 1 116 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 504 504 H -> HW (IN REF. 3).
 FT CONFLICT 610 616 LYSROR -> SUSNPPA (IN REF. 3).
 FT CONFLICT 742 742 A -> P (IN REF. 3).
 FT CONFLICT 786 786 V -> G (IN REF. 2).
 SQ SEQUENCE 813 AA; 29727267D7085845 CRC64;
 Query Match 17.6%; Score 479; DB 1; Length 813;
 Best Local Similarity 27.3%; Pred. No. 4.7e-24;
 Matches 143; Conservative 95; Mismatches 206; Indels 80; Gaps 19;
 QY 16 TSDYASV---VSNLFVALLCACIVLGLHLEE-NRWVNESITAIILIGLCYGVVILLMTKG 71
 DB 73 TLDYHVQVQPFETLWILLASAKIGFHYKLPITVPESCILLIMVGLLGGIIFGVDE- 131
 QY 72 KSHLFVSEDFEYLLPIIFNAGFOVKKOFFRNFMTITLFGAVGTMISFTTISIAA 131
 DB 132 KSPD--AMTDFVFLPPIVDAGYFMPTRPFENLGTIFWYAVVGTLMNSIGIGLSL 189
 QY 132 IAIFSRMNTGLDVG--DELAIGAIFSDVCTLOVL-NODETPFLYSLVFGGVVND 188
 DB 190 FGICQIEAFGLSDITLONLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGESLLND 249
 QY 189 TSIVLFLNALQNF-DLVHIDAADVVKELGNFFYFLSSTFLGVFAGLLSAY-----I 238
 DB 250 VTWVLYNLFKSCQMKTIQTVDFAGIANFVVGVLGGVILGILLGFIATFTTHNIRV 309
 QY 239 IKKLYIGRHSITREVALMMLAYLSYMLAELDLDSGLITVFCGIVMSHYTHNVTSSR 298
 DB 310 IEPLFV-----FLSYLTYITAEMLFHLGIMAITACAMTMKNKYVEENVQSQSY 357
 QY 299 VTKHAFATLSIAETFLFYVGMAL-DIEKWEFASDRPGKSGISSILLGLVLGIRAA 357
 DB 358 TTIKYMKMLSSVSETLIFIPMGVSTVCKNHEMNA-----FVCTFLAFLIWRAL 408
 QY 358 FVFPLSLNLTKKAPNEKITWROQVVIWAGLMRGAVSIATAY-----NKFTRSHTOLH 413
 DB 409 GVFLVTQVINFRITP---LTFKQDFIAYGGL-RGAICFALVFLLPATVFR----- 457
 QY 414 GNAIMITSTITVLFSTWVEGMMTKPLRLLLPASCHPVTSEPSPKSLHSLLTSMQGS 473
 DB 458 -KKLEITAAIVVFTFVILGITIRPLVEFLDVKRSN--KKQAAVSEEHICRFFDHVK-T 513
 QY 474 DLESTNIVRPFSSRLMLTKPHTVHYWR-----KFDDALMRPM 513
 DB 514 GIEDVCG-----HWGHNFRWROKFKFKDDKYLRKL 542
 RESULT 12
 NAHL_MOUSE
 ID NAHL_MOUSE
 AC Q61165;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
Sodium/hydrogen exchanger 1 (Na⁺/H⁺) exchanger 1) (NHE-1).
SLC9A1 OR NHE1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Dewey M.J., Bowman L.H.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -!- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; U51112; AAA92976.1; -
CC MGD; MG1:102462; SLC9A1.
CC InterPro; IPR000676; NaH_Exchange.
CC InterPro; IPR004709; NaH_exchange.
CC Pfam; PF00999; Na_H_Exchange; 1.
CC PRINTS; PR01084; NAHEXCHNGR.
CC TIGRfams; TIGR00840; b_cpai; 1.
CC Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
CC Multigene family; Phosphorylation.
CC DOMAIN 1 12
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 13 32
CC A (M1) HYDROPHOBIC.
CC DOMAIN 33 105
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 106 127
CC B (M2) HYDROPHOBIC.
CC DOMAIN 128 130
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 131 150
CC C (M3) (POTENTIAL).
CC TRANSMEM 151 162
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 163 183
CC D (M4) (POTENTIAL).
CC TRANSMEM 184 188
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 189 210
CC E (M5) (POTENTIAL).
CC TRANSMEM 211 230
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 231 251
CC F (M5A) (POTENTIAL).
CC TRANSMEM 252 260
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 261 282
CC G (M5B) (POTENTIAL).
CC TRANSMEM 283 301
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 302 322
CC H (M6) (POTENTIAL).
CC TRANSMEM 323 336
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 337 357
CC I (M7) (POTENTIAL).
CC TRANSMEM 358 388
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 389 410
CC J (M8) (POTENTIAL).
CC TRANSMEM 411 416
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 417 438
CC K (M9) (POTENTIAL).
CC TRANSMEM 439 452
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 453 473
CC L, HYDROPHOBIC.
CC TRANSMEM 474 482
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 483 503
CC M (M10) (POTENTIAL).
CC TRANSMEM 504 820
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 374 374
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD
CC SEQUENCE 820 AA; 91467 MW; 0589C4D08DD348BE CRC64;

Query Match

17.6%; Score 479; DB 1; Length 820;

Best Local Similarity 29.1%; Pred. No. 4.7e-24;
Matches 147; Conservative 98; Mismatches 202; Indels 58; Gaps 19;
QY 18 DYASV---V--INIFVALLCACIVLHLLER-NRWVNESITALLIGLCTGVVILLMKGKS 73
DB 99 DYHVRTPPFISILLACMLKGFHVIPTISSIVPECLLIIVVGLLVGLI---KGVG 154
QY 74 SHLFVSEDLFFIYLLPPIFNAGFOVKKQFFNFMTITLFGAVGTMTISFF--IAA 131
DB 155 ETTPFLQSDVFFLELLPIIDLAGYFLPLRQFTENLCTILIFAVVGTWNAFFLGLLYA 214
QY 132 IAFSRNIGTLDVGDFLAICAFSATDSVCTLOVLNQDE--TPFLSYLSVGEVVDNATS 190
DB 215 VCLVGGQINNIGLLDTLLFGSIISAVDPVAVLAFVEEIHINELLHLLVFGESILLDAVT 274
QY 191 IVLENALONF---DLVHDAAVLVKFLGNFFYFLSFLSTFLGVFAGLLSAYIIKKLYIGH 247
DB 275 VVLYHLEEFASYDSVGI--SDIFLGLF--SFFVVALGVGVVGVYVIAATSR---FTSH 329
QY 248 STDREVALMMLMAYSLMELDLSGLTVFFCGIVMHSVYTHNVTESSRVTTKHAFAT 307
DB 330 IRVIEPLEVLYSMAYLSAELFHLGIMALIASGVVMRYVEANISHKSHITIKYFLKM 389
QY 308 LSFTIAETFLDYVGMDAL-DIEKWFASDRPGKISIGISILLGLVLIGRAAFVPLSFLS 366
DB 390 WSSVSETLIFLFGVSTVAGSHOWNW-----TFVISTLL--FCLIAVLGLVLTWFI 440
QY 367 NLTKAPNEKITRQOVVIMWAGLARGAVSTALAYNKRTRSGHTQLHGNAMITSTTVV 426
DB 441 N---KFRIVUTPKDQFIATYAGGL--RGAIAFSLGY--LLDKKHPMCD--LFLTAITVI 492
QY 427 LFTSMVFGMTKPIRLILLPASGHPVTSEPSKSLSPSLTSMQGSDELSTTNIVRPSS 486
DB 493 FETVVGQMTIRPLVDLL-----AVKKQETKRSINEIHTQFLDHLLTGIEDIC---- 542
QY 487 LRMLLTKPTHTVHYWRKFDALMR 511
DB 543 -----GHYGHGHHWK---DKLAR 556
RESULT 13
NAH5_RAT ID NAH5_RAT STANDARD; PRT; 898 AA.
AC Q920X2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 5 (Na⁺/H⁺) exchanger 5) (NHE-5).
GN SLC9A5 OR NHE5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=99134373; PubMed=9933642;
RA Attaphitaya S., Park K., Melvin J.E.;
RT "Molecular cloning and functional expression of a rat Na⁺/H⁺ exchanger
RT (NHE5) highly expressed in brain";
RL J. Biol. Chem. 274:4383-4388(1999).
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----

FT DOMAIN 474 482 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 483 503 M (M10) (POTENTIAL).
FT DOMAIN 504 822 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 822 AA; 92003 MW; E97C1ACD4EB86DAA CRC64;

Query Match 17.6%; Score 478; DB 1; Length 822;
Best Local Similarity 28.7%; Pred. No. 5.5e-24;
Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;

QY 18 DYASV---VSNLFVALLCACIVLGHLEENRWNESITALIIGLCGVVILLMTKGS 73
DB 99 DQHVRIPEFETALWILLACLMKIGHPVIPTISSIVPESCLLVGLVGLI---KGVG 154
QY 74 SHLFVSEDLFFIYLLPPIINAGQVKKOFFRNMFTITLFGAVGTWISFTTIS--TAA 131
DB 155 ETPPLOSDFVFLPPIILDAGYFLPQFTENLGTILFVAVGTWLNFAFFLGGLLYA 214
QY 132 IAIFSRMNTIGLDVDFLAIGAFSATSVCVTQLVNODE--TPFLYSLVFGGVNDATS 190
DB 215 VCLVGEQINNGILLDTLLFGSIISAVDPVAVVAFEEIHINELLHILVFGESLLNDATV 274
QY 191 IVLFNALQ---NFDLVHDAVAVLKFGLNFFFLSFLGAVGAGLLSAYIIKKLYIGRH 247
DB 275 VVLYHLFEFANYDSTGI--SDIFLGLF--SFFVVALGGVFGVYGVIAFTSR---FTSH 329
QY 248 STDREVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMSHYTMHNVTSSRVTTKHAFAT 307
DB 330 IRVIEPLFVLSYMAISAEFLHSLGIMALIASGVMPVYVEANISHKSHHTTKIFLKM 389
QY 308 LSFIAETFLFVGVGDAL--DIEKWEFASDPGKSGISILLGLVLIGRAAFVFLPLSLS 366
DB 390 WSSVSETLIFLGVSTVAGSHQWNN-----TFVISILL--FGLIARVLGLVLTWFI 440
QY 367 NLTKKAPNEKITRQOVVITWAGLMRGAVSIALATNKFTRSGHTQIHGNAMITITIVV 426
DB 441 N---KPRIVKTPKQFIAYGGL--RGATAFSLGY--LMDKKHFPMD--LFLTAITIVI 492
QY 427 LFTMTVFGMTKPLIRLLPASGHPVTSBPSPKSLHSPLLTSMQGSDELTNTVVRPSS 486
DB 493 FTFVVGQMTIRPLVDLL-----AVKKQETKRSINEIHTQFLDHLTLGTEDIC---- 542
QY 487 LRMLLTKPHTHYVYWRKEDDALMR 511
DB 543 -----GHYGHWHK-----DKLNR 556

PRT: 817 AA.

RESULT 15
ID NAHL_BOVIN STANDARD; PRT: 817 AA.
AC Q28036;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 1 (Na(+)/H(+)) exchanger 1) (NHE-1).
GN SLC9A1 OR NHE1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Zhu H., Zhang Q., Zhang X., Liu W., Trumbly R.J., Garlid K.D.,
RA Sun X.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -!- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U49432; AAA91483.1; --
DR InterPro: IPR000676; NaH_Exchange.
DR InterPro: IPR004709; NaH_Exchange3.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR PRINTS: PR01084; NAEXCHNGR.
DR TIGRFAMs: TIGR00840; b_cpai; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
KW Multigene family; Phosphorylation.
DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 16 35 M1 (POTENTIAL).
FT DOMAIN 36 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 127 M2 (POTENTIAL).
FT DOMAIN 128 129 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 130 149 M3 (POTENTIAL).
FT DOMAIN 150 154 M4 (POTENTIAL).
FT TRANSMEM 155 174 M5 (POTENTIAL).
FT DOMAIN 175 191 M5 (POTENTIAL).
FT TRANSMEM 192 211 M5 (POTENTIAL).
FT DOMAIN 212 227 M5A (POTENTIAL).
FT TRANSMEM 228 247 M5B (POTENTIAL).
FT DOMAIN 248 256 M5B (POTENTIAL).
FT TRANSMEM 257 276 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 277 294 M6 (POTENTIAL).
FT TRANSMEM 295 315 M6 (POTENTIAL).
FT DOMAIN 316 338 M7 (POTENTIAL).
FT TRANSMEM 339 358 M7 (POTENTIAL).
FT DOMAIN 359 386 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 387 406 M8 (POTENTIAL).
FT DOMAIN 407 410 M9 (POTENTIAL).
FT TRANSMEM 411 430 M9 (POTENTIAL).
FT DOMAIN 431 480 M10 (POTENTIAL).
FT TRANSMEM 481 500 M10 (POTENTIAL).
FT DOMAIN 501 817 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 817 AA; 91017 MW; 6617E99D3B012920 CRC64;

Query Match 17.5%; Score 476; DB 1; Length 817;
Best Local Similarity 28.8%; Pred. No. 7.4e-24;
Matches 146; Conservative 98; Mismatches 201; Indels 62; Gaps 19;

QY 18 DYASV---VSNLFVALLCACIVLGHLEENRWNESITALIIGLCGVVILLMTKGS 73
DB 95 DQHVRIPEFETALWILLACLMKIGHPVIPTISSIVPESCLLVGLVGLI---KGVG 150
QY 74 SHLFVSEDLFFIYLLPPIINAGQVKKOFFRNMFTITLFGAVGTWISFTTIS--TAA 131
DB 151 ETPPLOSDFVFLPPIILDAGYFLPQFTENLGTILFVAVGTWLNFAFFLGGLLYA 210
QY 132 IAIFSRMNTIGLDVDFLAIGAFSATSVCVTQLVNODE--TPFLYSLVFGGVNDATS 190
DB 211 VCLVGEQINNGILLDTLLFGSIISAVDPVAVVAFEEIHINELLHILVFGESLLNDATV 270
QY 191 IVLFNALQ---NFDLVHDAVAVLKFGLNFFFLSFLGAVGAGLLSAYIIKKLYIGRH 247
DB 271 VVLYHLFEFANYDSTGI--SDIFLGLF--SFFVVALGGVFGVYGVIAFTSR---FTSH 325
QY 248 STDREVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMSHYTMHNVTSSRVTTKHAFAT 307


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Db 326 IRVIEPLFVFLYSMAYLSAELPHLSGIMALTASGVVMPYVEANISHKSHTTIKYFLKM 385
QY 308 LSFIAETFLFLXVGMALDIE---KWEFASDRPGKSIGISSILLGIVLIGRAAFVPLSF 364
Db 386 WSSVSETLIFLGVSTVAGSHHWNWTFV-----ISTLL--FCLLARVLGVLGLTW 434
QY 365 LSNLTKKAPNEKITWRQOVVIWAGLMRGAVSIALAYNNKFTRSQHTQLHGNAMITSTYT 424
Db 435 FIN---KFRIVKLTPKDOPFIAYGGI--RGAIAPSLGY--LLDKKHFPMD--LFLTAIIT 486
QY 425 VVLFSTWVFGMMTKPLIRLLLPASGHPVISEPSPKSLHSPLLTSMOGSDLESTTNIVRP 484
Db 487 VIFFTFVOGMITRPLVDLL-----AVKKKQETKRSINEEHTQFLDHLTLTGIEDIC-- 538
QY 485 SSLRMLLTAKPTHVHYWYWRKFDLALMR 511
Db 539 -----GHYCHHMK---DKLNR 552

```

Search completed: March 26, 2003, 18:53:06
Job time : 34 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:49:39 ; Search time 38 Seconds
(without alignments)
2900.926 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAARLALYTTSDYA.....GRGFVPFSPCSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2722	100.0	535	10	Q9SXJ8		Q9sxj8 oryza sativ
2	2105.5	77.4	555	10	Q9FZM0		Q9fzn0 atriplex gm
3	2103.5	77.3	540	10	Q94LX5		Q94lx5 petunia hyb
4	2095.5	77.0	553	10	Q94LX4		Q94lx4 nierenbergi
5	2080	76.4	546	10	Q9CAW6		Q9caw6 arabidopsis
6	2065.5	75.9	542	10	Q94IE0		Q94ie0 ipomoea tri
7	2055.5	75.5	542	10	Q9FEB3		Q9feb3 pharbitis n
8	2054.5	75.5	556	10	Q94K25		Q94k25 suaeda mari
9	2043	75.1	542	10	Q9ARH6		Q9arh6 citrus para
10	2023.5	74.3	538	10	Q9ZPK3		Q9zpk3 arabidopsis
11	1966	72.2	555	10	Q94LX3		Q94lx3 torenia hyb
12	1931	70.9	552	10	Q9SQU0		Q9squ0 arabidopsis
13	1921.5	70.6	546	10	Q94BM4		Q94bm4 triticum ae
14	1879	69.0	534	10	Q93YH2		Q93yh2 lycopersico
15	1698.5	62.4	457	10	O04G55		O04g55 arabidopsis
16	1529	56.2	529	10	Q9FJ63		Q9fj63 arabidopsis

17	1529	56.2	529	10	Q8S397		Q8s397 arabidopsis
18	1356	49.8	295	10	Q94BM3		Q94bm3 triticum ae
19	619	22.7	576	11	Q8R4D1		Q8r4d1 mus musculu
20	595.5	21.9	561	5	Q9XZM4		Q9xzm4 drosophila
21	595.5	21.9	649	5	Q9VPI1		Q9vpj1 drosophila
22	592.5	21.8	649	5	Q8SZX8		Q8szx8 drosophila
23	579.5	21.3	611	5	Q8T5R7		Q8t5r7 caenorhabdi
24	579.5	21.3	630	5	Q8T5R8		Q8t5r8 caenorhabdi
25	569	20.9	687	5	Q9U624		Q9u624 drosophila
26	567.5	20.8	629	5	Q20944		Q20944 caenorhabdi
27	565	20.8	727	5	Q9VM99		Q9vm99 drosophila
28	564.5	20.7	655	5	Q8T5R3		Q8t5r3 caenorhabdi
29	564.5	20.7	681	5	Q8T5R4		Q8t5r4 caenorhabdi
30	564.5	20.7	703	5	Q9XW14		Q9xw14 caenorhabdi
31	558.5	20.5	517	10	Q8S396		Q8s396 arabidopsis
32	553	20.3	725	4	Q96T83		Q96t83 homo sapien
33	552	20.3	569	3	O13726		O13726 schizosacch
34	551	20.2	531	10	Q93YH1		Q93yh1 lycopersico
35	546	20.1	525	10	Q8S395		Q8s395 arabidopsis
36	545	20.0	535	10	Q8RWU6		Q8rwu6 arabidopsis
37	533	19.6	140	10	Q9LKH5		Q9lkh5 mesembryant
38	528	19.4	153	10	Q9LKH6		Q9lkh6 mesembryant
39	513	18.8	106	10	Q9ATZ9		Q9atz9 zea mays (m
40	497.5	18.3	437	4	Q9Y507		Q9y507 homo sapien
41	488.5	17.9	560	3	Q9HEX3		Q9hex3 pneumocysti
42	475.5	17.5	518	5	Q9VIF9		Q9vif9 drosophila
43	475.5	17.5	582	5	Q8WPH4		Q8wph4 drosophila
44	467	17.2	1203	5	Q9NGZ4		Q9ngz4 drosophila
45	459.5	16.9	1179	5	Q9NCQ0		Q9ncq0 aedes aegyp

ALIGNMENTS

RESULT 1

Q9SXJ8	ID	Q9SXJ8	PRELIMINARY:	PRT;	535 AA.
AC	Q9SXJ8;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)				
DE	OSNHX1 protein.				
GN	OSNHX1.				
OS	Oryza sativa (Rice).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Ehrhartoideae; Oryzeae; Oryza.				
OX	NCBI_TaxID=4530;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. NIPPONBARE;				
RX	MEDLINE=93326147; PubMed=10395929;				
RA	Fukuda A., Nakamura A., Tanaka Y.;				
RT	"Molecular cloning and expression of the Na+/H+ exchanger gene in Oryza sativa.";				
RL	Biochim. Biophys. Acta 1446:149-155(1999).				
DR	EMBL; AB021878; BAA83337.1; .				
DR	InterPro; IPR004709; NaH_exchang3.				
DR	InterPro; IPR000676; NaH_Exchange1.				
DR	Pfam; PF00999; Na_H_Exchange; 1.				
DR	PRINTS; PR01084; NAHEXCHNGR.				
DR	TIGRFAMS; TIGR00840; b_cpai; 1.				
SQ	SEQUENCE 535 AA; 6BCADB29B131976 CRC64;				

Query Match	100.0%;	Score 2722;	DB 10;	Length 535;
Best Local Similarity	100.0%;	Pred. No. 7.4e-193;		
Matches 535;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGMEVAARLALYTTSDYASVWSINLFLVALLCACIVLGHLLLEENRWVNESITALIIGLC 60		
Db	1	MGMEVAARLALYTTSDYASVWSINLFLVALLCACIVLGHLLLEENRWVNESITALIIGLC 60		
Qy	61	TGVVILLMTKCKSSHLVFESEDLFFIYLLPPIIFNAGFOVKKOFFRNFMTITLFGAVGT 120		

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Db 61 TGVVILLMTKSSHLVFSEDLFFIYLLPPIIFNAGFOVKKQFRFMFTTLFCVAGVT 120
QY 121 MISFETISIAAIAIFSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVLNODETPFYLSLVF 180
Db 121 MISFETISIAAIAIFSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVLNODETPFYLSLVF 180
QY 181 GEGVNDATSIYLFNALQNFOLVHIDAADVVKFLGNFFYFLFUSSTFLGVFAGLLSAYIIK 240
Db 181 GEGVNDATSIYLFNALQNFOLVHIDAADVVKFLGNFFYFLFUSSTFLGVFAGLLSAYIIK 240
QY 241 KLYIGRHSSTDREVALMMLMAYLSYMLAELLDLSGLTFFFCGIVMSHYTHWNVTSSRYT 300
Db 241 KLYIGRHSSTDREVALMMLMAYLSYMLAELLDLSGLTFFFCGIVMSHYTHWNVTSSRYT 300
QY 301 TKHAPATLSIAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVF 360
Db 301 TKHAPATLSIAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVF 360
QY 361 PLSFSLNLTKKAPNEKITRWQOVVIVWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMIT 420
Db 361 PLSFSLNLTKKAPNEKITRWQOVVIVWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMIT 420
QY 421 STITVLFSTVWFGMTKPLIRLLPASGHPVTSPPSPKSLHSPLLTSMOGSDLESTTN 480
Db 421 STITVLFSTVWFGMTKPLIRLLPASGHPVTSPPSPKSLHSPLLTSMOGSDLESTTN 480
QY 481 IVRPSSRLMLTKPHTVHYWYRKFDALMRPFGRGVFPFSPGSPTEQSHGGR 535
Db 481 IVRPSSRLMLTKPHTVHYWYRKFDALMRPFGRGVFPFSPGSPTEQSHGGR 535

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RESULT 2

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Q9FZNO PRELIMINARY: PRT; 555 AA.
AC Q9FZNO;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Na/H antiporter Nhx1.
GN AGNHX1.
OS Atriplex gmelini.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Atriplex.
OX NCBI_TaxID=118074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21330247; PubMed=11437248;
RA Hamada A., Shono M., Xia T., Ohta M., Hayashi Y., Tanaka A.,
RA Hayakawa T.
RT "Isolation and characterization of a Na+/H+ antiporter gene from the
RT halophyte Atriplex gmelini."
RL Plant Mol. Biol. 46:35-42(2001).
DR EMBL; AB038492; BAB11940.1; -
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 555 AA; 61504 MW; ACD5ED45FF3D398A CRC64;

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Query Match 77.4%; Score 2105.5; DB 10; Length 555;
Best Local Similarity 76.8%; Pred. No. 2.3e-147;
Matches 410; Conservative 53; Mismatches 61; Indels 15; Gaps 4;

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QY 7 AARLGALYTTSDXASVSYNLFVALLCIVGLHLLERNRWNESITALIIGCTGVVIL 66
Db 10 SGRMDAL-TTSDHASVSYNLFVALLCIVGLHLLERNRWNESITALIIGCTGVVIL 68
QY 67 LMTYKSSHLVSEDLFFIYLLPPIIFNAGFOVKKQFRFMFTTLFCVAGTMSIFFT 126
Db 69 LISGGKSSHLVSEDLFFIYLLPPIIFNAGFOVKKQFRFMFTTLFCVAGTMSIFFT 128

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QY 127 ISTAIAIAIFSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVLNODETPFYLSLVF 186
Db 129 ISUGALSIFKLDIGTLEADYLAIGAIPAANDSVCTLOVLNODETPFYLSLVF 188
QY 187 DATSVLFNALQNFOLVHIDAADVVKFLGNFFYFLFUSSTFLGVFAGLLSAYIIKLYIGR 246
Db 189 DATSVLFNALQNFOLVHIDAADVVKFLGNFFYFLFUSSTFLGVFAGLLSAYIIKLYIGR 248
QY 247 HSTDREVALMMLMAYLSYMLAELLDLSGLTFFFCGIVMSHYTHWNVTSSRYT 306
Db 249 HSTDREVALMMLMAYLSYMLAELLDLSGLTFFFCGIVMSHYTHWNVTSSRYT 308
QY 307 TLSFIAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVF 366
Db 309 TLSFIAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVF 368
QY 367 NLTKAPNEKITRWQOVVIVWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMIT 426
Db 369 NFAKKSQSEKVTNFQOIVWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMIT 428
QY 427 LFTMVFGMTKPLIRLLPASGHPVTSPPSPKSLHSPLLTSMOGSDL----- 475
Db 429 LFTMVFGMTKPLIRLLPASGHPVTSPPSPKSLHSPLLTSMOGSDL----- 488
QY 476 ESTT---NIVRPSSRLMLTKPHTVHYWYRKFDALMRPFGRGVFPFSPGSPTEQS 531
Db 489 EDTTEPTIVRPSSRLMLLNAPHTVHYWYRKFDALMRPFGRGVFPFSPGSPTEQS 547

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RESULT 3

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Q94LX5 PRELIMINARY: PRT; 540 AA.
AC Q94LX5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Na H-antiporter.
GN PHUPRPLE.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;
RT "Plant Na-H antiporter."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051817; BAB56105.1; -
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR000676; Na_H_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 540 AA; 59510 MW; BCE2740F275E896A CRC64;

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Query Match 77.3%; Score 2103.5; DB 10; Length 540;
Best Local Similarity 77.4%; Pred. No. 3.2e-147;
Matches 404; Conservative 53; Mismatches 62; Indels 3; Gaps 1;

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QY 15 TTSDYASVSYNLFVALLCIVGLHLLERNRWNESITALIIGCTGVVILMTKGS 74
Db 16 TSDHQSVSYNLFVALLCIVGLHLLERNRWNESITALVIGSCTGIVILLISG 75
QY 75 HLFVSEDLFFIYLLPPIIFNAGFOVKKQFRFMFTTLFCVAGTMSIFTAATAI 134
Db 76 HLFVSEDLFFIYLLPPIIFNAGFOVKKQFRFMFTTLFCVAGTMSIFTAATAI 135
QY 135 FSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVLNODETPFYLSLVF 194
Db 136 FKKMNIQSLEIGDYLAIGAIFSAITSDSVCTLOVLNODETPFYLSLVF 195
QY 195 NALQNFOLVHIDAADVVKFLGNFFYFLFUSSTFLGVFAGLLSAYIIKLYIGR 254

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Db 196 NAIQNFDSLHDTGKAMELVGNFLYLAFASSTALGVAAGLLSAYIIKKLYFGHSTDEVA 255
Qy 255 LMLMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAET 314
Db 256 IMILMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAEI 315
Qy 315 FELYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFLSFLSNLTKKAPN 374
Db 316 FELYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFLSFLSNLTKKAPN 375
Qy 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTSRGHTOLHGNAMITSTITVVLFSFVVF 434
Db 376 DKISFNQOVTIWWAGLMRGAVSMALAYNQFTRGHTQLRANAMITSTITVVLFSFVVF 435
Qy 435 MMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMOGSDLESTTNIVRPSLRMLL 491
Db 436 LMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMOGSDLESTTNIVRPSLRMLL 495
Qy 492 TKPHTVHYWYRKFDALMRPFGGRGVFPFSGSPTEOSH 533
Db 496 STPSTVHYWYRKFDALMRPFGGRGVFPFSGSPTEOVGG 537

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RESULT 4
Q94LX4
ID Q94LX4 PRELIMINARY; PRT: 553 AA.
AC Q94LX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Na H-antiporator.
CN NHPURPLE.
OS Nierembergia caerulea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nierembergia.
OX NCBI_TaxID=144865;
RN [1]
RP SEQUENCE FROM N.A.
RA Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;
RT "Plant Na-H antiporator."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB051818; BAB56106.1;
DR InterPro: IPR001179; FKBP_Pptase.
DR InterPro: IPR004709; NaH_exchng3.
DR InterPro: IPR000676; NaH_exchng1.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR TIGRFAMs: TIGR00840; b_Cpal; 1.
DR PROSITE: PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 553 AA; 61119 MW; 9F2B47A49D7AB2CC CRC64;

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Query Match 77.0%; Score 2095.5; DB 10; Length 553;
Best Local Similarity 77.8%; Pred. No. 1.3e-146;
Matches 403; Conservative 49; Mismatches 63; Indels 3; Gaps 1;

Qy 15 TTSDYASVYVNSLNFVALLCAGTIVGLHLEENRWNESITALIGLCTGWTLLMTKGRSS 74
Db 16 TTSDHQSVVSNLNFVALLCAGTIVGLHLEENRWNESITALVIGSCTGVIIILISGCKNS 75
Qy 75 HLEFVSEDLFFTYLLPPIIFNAGFOVKKQFRNFWITLFGAVGTMISFFTTIAATAI 134
Db 76 HILVSEDLFFTYLLPPIIFNAGFOVKKQFRNFWITLFGAVGTMISFFTTIAATAI 135
Qy 135 FSRMNGTLVDGDLAIGAFISATSVCTQLVNLQDETFPLYSLVFGGVNDATSVILF 194
Db 136 FKMDIGHLEIGDYLGAIFAATSVCTQLVNLQDETFPLYSLVFGGVNDATSVILF 195
Qy 195 NALQNFDLVHDAVVAFLNFFGLFSLTSFLGVFAGLLSAYIIKKLYIGHSTDEVA 254
Db 196 NAVQNFDSLHDTGKAMELVGNFLYLAFASSTALGVAAGLLSAYIIKKLYFGHSTDEVA 255
Qy 255 LMLMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAET 314

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Db 256 IMILMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAEI 315
Qy 315 FELYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFLSFLSNLTKKAPN 374
Db 316 FELYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFLSFLSNLTKKAPN 375
Qy 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTSRGHTOLHGNAMITSTITVVLFSFVVF 434
Db 376 DKISFNQOVTIWWAGLMRGAVSMALAYNQFTRGHTQLRANAMITSTITVVLFSFVVF 435
Qy 435 MMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMOGSDLESTTNIVRPSLRMLL 491
Db 436 LMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMOGSDLESTTNIVRPSLRMLL 495
Qy 492 TKPHTVHYWYRKFDALMRPFGGRGVFPFSGSPTE 529
Db 496 STPSTVHYWYRKFDALMRPFGGRGVFPFSGSPTE 533

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RESULT 5
Q9CAW6
ID Q9CAW6 PRELIMINARY; PRT: 546 AA.
AC Q9CAW6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative sodium proton exchanger (Na+/H+ exchanger 2).
GN T9J14.2 OR NHX2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brothier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharte M., Schoen O., Barques M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liquori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Otterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Millscher J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Iwasawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinjo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana.";
RL Nature 408:820-822(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yokoi S., Quintero F.J., Cubero B., Ruiz T., Bressan R.A.,
RA Hasegawa P.M., Pardo J.M.;
RT "Differential expression and function of Arabidopsis thaliana NHX Na+/H+ antiporters in the salt stress response.";

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RL Plant J. 0-0-0(2002).
DR EMBL; AF009465; AAG51408.1; -.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR004709; NaH_exchang3.
DR InterPro; IPR000676; NaH_exchng1.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR TIGRFAMs; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN.1.
SQ SEQUENCE 546 AA; 60522 MW; BEA270D04046360B CRC64;

Query Match 76.4%; Score 2080; DB 10; Length 546;
Best Local Similarity 76.6%; Pred. No. 1.7e-145;
Matches 402; Conservative 54; Mismatches 61; Indels 8; Gaps 2;

QY 15 TSDYASVVSINLFVALLCACIVLGHLEENRWNESITALIIGLCTGVVILLMTKGSS 74
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 15 STSDHASVVSINLFVALLCACIVLGHLEENRWNESITALIIGLCTGVVILLMTKGSS 74
QY 75 HLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFGAVGTMISFFETISAAIAI 134
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 75 HLLVSEDLFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFGAVGTMISFFETISAAIAI 134
QY 135 FSRMNIIGTLDVGDFLAIGAIFSATDSVCTLOVLNODETPFYLSLVFGGVNDATSI 194
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 135 FKLLDGTGDFLGDFLAIGAIFAAATDSVCTLOVLNODETPFYLSLVFGGVNDATSI 194
QY 195 NALQNFDLVHIDAAVVLKFLGNFFYLFSLTFLGVFAGLLSAYIIKKLYIGHSTDEVA 254
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 195 NAIQSFDTLHNEAAFOGLGNFFYLFSLTFLGVATGLISAYIIKKLYIGHSTDEVA 254
QY 255 LMMLMAYLSYMLAELLDLSGLITVFFCGIVMSHYTHWNTVESSRVTTKHAFATLSFAET 314
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 255 LMMLMAYLSYMLAELFALSGLITVFFCGIVMSHYTHWNTVESSRVTTKHAFATLSFAET 314
QY 315 FLFYVGMADLDIEKWEFASDPKSGISGISTLLGLVLIGRAAFVPLSFLSLNLTAKPNE 374
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 315 FIFYVGMADLDIEKWEFASDPKSGISGISTLLGLVLIGRAAFVPLSFLSLNLTAKPNE 374
QY 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTRSRGTOLHGNAMITSTITVVLFSFWMFG 434
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 375 EKISIKOOVVIWAGLMRGAVSMALAYNKFTRSRGTOLHGNAMITSTITVVLFSFWMFG 434
QY 435 MTKPLIRLLLP-----ASGHPVTSPPSKLSHSLPILTSMQGSDLE---STTNIVRPS 486
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 435 MLTKPLIRLLLP-----ASGHPVTSPPSKLSHSLPILTSMQGSDLE---STTNIVRPS 486
QY 487 LRMLLTPTHTVHYWKRKFDALMRPFGGRGVFPSPGSPTEQS 531
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 495 LRGLMRPTHTVHYWKRKFDALMRPFGGRGVFPSPGSPTEQS 539

RESULT 6
Q94IEO PRELIMINARY; PRT; 542 AA.
AC Q94IEO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Na+/H+ exchanger.
GN T[HN]X1.
OS Ipomoea tricolor (Morning glory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=89664;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21276661; PubMed=11382810;
RA Yamaguchi T., Fukada-Panaka S., Inagaki Y., Saito N., Iida S.;
RA Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.;
RT "Genes Encoding the Vacuolar Na+/H+ Exchanger and Flower Coloration.";
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RL Plant Cell Physiol. 42:451-461(2001).
DR EMBL; AB054979; BAB60901.1; -.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR004709; NaH_exchang3.
DR InterPro; IPR000676; NaH_exchng1.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN.1.
SQ SEQUENCE 542 AA; 60024 MW; OC8381CFB78B239C CRC64;

Query Match 75.9%; Score 2065.5; DB 10; Length 542;
Best Local Similarity 76.6%; Pred. No. 2e-144;
Matches 402; Conservative 50; Mismatches 64; Indels 9; Gaps 3;

QY 16 TSDYASVVSINLFVALLCACIVLGHLEENRWNESITALIIGLCTGVVILLMTKGSSH 75
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 16 TSDHASVVSINLFVALLCACIVLGHLEENRWNESITALIIGLCTGVVILLMTKGSSH 75
QY 76 LHFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFGAVGTMISFFETISAAIAIF 135
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 76 LHFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNFMTITLFGAVGTMISFFETISAAIAIF 135
QY 136 SRMNIIGTLDVGDFLAIGAIFSATDSVCTLOVLNODETPFYLSLVFGGVNDATSI 195
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 136 KHLDDTDFLGDFLAIGAIFAAATDSVCTLOVLNODETPFYLSLVFGGVNDATSI 195
QY 196 ALQNFDFLHIDAAVVLKFLGNFFYLFSLTFLGVFAGLLSAYIIKKLYIGHSTDEVAL 255
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 196 ALQSFDTLHNEAAFOGLGNFFYLFSLTFLGVGIGLLCAYIIKKLYIGHSTDEVAL 255
QY 256 LMMLMAYLSYMLAELLDLSGLITVFFCGIVMSHYTHWNTVESSRVTTKHAFATLSFAET 315
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 256 LMMLMAYLSYMAELFALSGLITVFFCGIVMSHYTHWNTVESSRVTTRHSFATLSFAET 315
QY 316 FLFYVGMADLDIEKWEFASDPKSGISGISTLLGLVLIGRAAFVPLSFLSLNLTAKPNE 375
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 316 FLFYVGMADLDIEKWEFASDPKSGISGISTLLGLVLIGRAAFVPLSFLSLNLTAKPNE 375
QY 376 KITWROQVVIWAGLMRGAVSIALAYNKFTRSRGTOLHGNAMITSTITVVLFSFWMFG 435
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 376 KISFQQIIVWAGLMRGAVSIALAYNKFTSGHPSLHENAIMITSTVTVLFSFVVL 435
QY 436 MTKPLIRLLLP-----ASGHPVTSPPSKLSHSLPILTSMQGSDLESTT--NIVRPS 486
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 436 MTKPLIRLLLP-----ASGHPVTSPPSKLSHSLPILTSMQGSDLESTT--NIVRPS 486
QY 487 LRMLLTPTHTVHYWKRKFDALMRPFGGRGVFPSPGSPTEQS 531
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 496 LRMLLTPTHTVHYWKRKFDALMRPFGGRGVFPSPGSPTEQS 540

RESULT 7
Q9FEB3 PRELIMINARY; PRT; 542 AA.
AC Q9FEB3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Na+/H+ exchanger (Na+/H+ exchanger protein).
GN PURPLE OR INNHX1.
OS Pharbitis nil (Violet) (Japanese morning glory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35883;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=KKZSK-2; TISSUE=LEAF, AND FULLY COLORED FLOWER BUDS;
RX MEDLINE=20487008; PubMed=11034195;
RA Fukada-Tanaka S., Inagaki Y., Yamaguchi T., Saito N., Iida S.;
RT "Colour-enhancing protein in blue petals.";
RN [2]
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RP SEQUENCE FROM N.A.
RC STRAIN=PR-R; TISSUE=LEAF;
RA MEDLINE=21276661; PubMed=11382810;
RX Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N.,
RA Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.;
RT "Genes Encoding the Vacuolar Na+/H+ Exchanger and Flower Coloration.";
RL Plant Cell Physiol. 42:451-461(2001).
DR EMBL; AB033990; BAB16381.1; -
DR EMBL; AB033989; BAB16380.1; -
DR EMBL; AB055062; BAB60899.1; -
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR004709; Nah_Exchange3.
DR InterPro; IPR000676; Nah_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR TIGRFAMS; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
SQ SEQUENCE 542 AA; 59973 MW; 4B47FDE04401A191 CRC64;

Query Match 75.5%; Score 2055.5; DB 10; Length 542;
Best Local Similarity 76.4%; Pred. No. 1.4e-143;
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;

QY 16 TSDASVVSINFLVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGKSSH 75
DB 16 TSDASVVSINFLVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGKSSH 75

QY 76 LFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAIAIF 135
DB 76 LFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAIAIF 135

QY 136 SRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVLNODETPFYLSLVFGGVNDATSVILFN 195
DB 136 SRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVLNODETPFYLSLVFGGVNDATSVILFN 195

QY 196 ALQNFDLVHDAVVLKFLGNFFLFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDEVAL 255
DB 196 ALQNFDLVHDAVVLKFLGNFFLFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDEVAL 255

QY 256 NMLMAYLSYMAELDLGLTVPFCGIVMHSYTHWNVTSSRVTTKHAFTATLSFIAFTF 315
DB 256 NMLMAYLSYMAELDLGLTVPFCGIVMHSYTHWNVTSSRVTTKHAFTATLSFIAFTF 315

QY 316 LFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTKAPNE 375
DB 316 LFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTKAPNE 375

QY 376 KITRQVQVIVWAGLMRGAVSIALAYNKFTRSHTQLHGNAMITSTITVVLFSTVFGM 435
DB 376 KITRQVQVIVWAGLMRGAVSIALAYNKFTRSHTQLHGNAMITSTITVVLFSTVFGM 435

QY 436 MTKPLIRLLP-----ASGHP--VTSEPPSPKSLHSPLLTSMQSGDLESTT--NIVRPSS 486
DB 436 MTKPLIRLLP-----ASGHP--VTSEPPSPKSLHSPLLTSMQSGDLESTT--NIVRPSS 486

QY 487 LRMLLTKPTHVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 531
DB 487 LRMLLTKPTHVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 531

QY 496 LRMLLTKPTHVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 540
DB 496 LRMLLTKPTHVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 540

RESULT 8
Q94K25 ID Q94K25 PRELIMINARY; PRT; 556 AA.
AC Q94K25;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Nat+/H+ antiporter.
OS Suaeda maritima subsp. salsa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Suaeda.
OX NCBI_TaxID=126914;

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RN SEQUENCE FROM N.A.
RP Zhang H., Zhang Q., Ma X.;
RT "Na+/H+ antiporter in Suaeda salsa.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF370358; AAK53432.1; -
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR004709; Nah_Exchange3.
DR InterPro; IPR000676; Nah_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMS; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
SQ SEQUENCE 556 AA; 61672 MW; DDF6AB696647D48E CRC64;

Query Match 75.5%; Score 2054.5; DB 10; Length 556;
Best Local Similarity 74.2%; Pred. No. 1.4e-143;
Matches 395; Conservative 56; Mismatches 68; Indels 13; Gaps 2;

QY 13 LYTTSDYASVVSINFLVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGK 72
DB 13 LYTTSDYASVVSINFLVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGK 72

QY 73 SSSLVFESEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAI 132
DB 73 SSSLVFESEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAI 132

QY 133 AIFSRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVLNODETPFYLSLVFGGVNDATSV 192
DB 133 AIFSRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVLNODETPFYLSLVFGGVNDATSV 192

QY 193 LFNALQNFDLVHDAVVLKFLGNFFLFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDE 252
DB 193 LFNALQNFDLVHDAVVLKFLGNFFLFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDE 252

QY 253 VALMMLMAYLSYMAELDLGLTVPFCGIVMHSYTHWNVTSSRVTTKHAFTATLSFIA 312
DB 253 VALMMLMAYLSYMAELDLGLTVPFCGIVMHSYTHWNVTSSRVTTKHAFTATLSFIA 312

QY 313 ETFLFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTKKA 372
DB 313 ETFLFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTKKA 372

QY 373 PNEKITRQVQVIVWAGLMRGAVSIALAYNKFTRSHTQLHGNAMITSTITVVLFSTV 432
DB 373 PNEKITRQVQVIVWAGLMRGAVSIALAYNKFTRSHTQLHGNAMITSTITVVLFSTV 432

QY 433 FGMATKPLIRLLP-----PVTSEPPSPKSLHSPLLTSMQSGDLESTN----- 480
DB 433 FGMATKPLIRLLP-----PVTSEPPSPKSLHSPLLTSMQSGDLESTN----- 480

QY 481 -IVRPSSLRMLTKPTHVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 531
DB 481 -IVRPSSLRMLTKPTHVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 531

QY 495 TIARPTSLRMLLNAPTHTVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 546
DB 495 TIARPTSLRMLLNAPTHTVHYWRKFDALMRPMFGGGRGVFPSPGSPTEQS 546

RESULT 9
Q9ARH6 ID Q9ARH6 PRELIMINARY; PRT; 542 AA.
AC Q9ARH6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Sodium/proton exchanger.
OS Citrus paradisi (Grapefruit).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=37656;
RN SEQUENCE FROM N.A.
RP TISSUE=PEEL;
RC Porat R., Lurie S., Povancello D.;
RA "A heat treatment induced the transcription of a sodium proton
RT

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RT	exchanger gene in grapefruit peel tissue.";
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY028416; AAK27314.2; -
DR	InterPro; IPR001179; FKBP_PP1ase.
DR	InterPro; IPR004709; NaH_Exchng3.
DR	InterPro; IPR000676; NaH_ExchngR.
DR	Pfam; PFO0999; Na_H_ExchangeR; 1.
DR	PRINTS; PR01084; NAHEXCHNGR.
DR	TIGRFRAMS; TTGR00840; b_cpai1; 1.
DR	PROSITE; PS00453; FKBP_PP1ASE_1; UNKNOWN_1.
SQ	SEQUENCE 542 AA; 59836 MW; 1A8525F2C5FAPE2C CRC64;

Query Match 75.1%; Score 2043; DB 10; Length 542;
Best Local Similarity 74.3%; Pred. No. 9.3e-143;
Matches 394; Conservative 57; Mismatches 71; Indels 8; Caps 4;

QY	13	LYTTSYASVSWINLFWALLCACIVLGHLLEENRWNNESITALLIGLCITGVILLMTGK	72
	:	: :	
Db	14	MVNTSDHNSVWSINIFVALPCASIVIGHLLLESRWNNESITALLIGVCACVILLTTGGK	73

[illegible]

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QY      133  AIFSRMNI GTLDV GDF LAI GAIFA SATDSV CTQLV NQDET PLYSLVFEGGVNDATSV 192
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      134  OFFKKLDIGTLDIGDY LAI GAIFAATDSVCTQLV NQDDTPIYSLVFEGGVNDATSV 193

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QY      193  LFNALQNFDLVHIDAANVLKFLGNFFYLFUSSTFLGVFAGLLSAYITKKLYIGRHSTDR 252
      |||||+||| ||| :||| ||| ||| ||| |||||+||| |||||
Db      194  LFNAIOSFDLTHNTRSAPOFIGNFLYIPRTSTLIVGIGIISAVUTKIVVEGDSMDRE 253

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Oy	253	VALMMLAYLSYMLAELDLGSLITVFFCGIVMSHYTWHNTESSRVTTKHAFAATLSFIA	312
		: :	
Dh	254	VALMMLAVI SVMI AEI EVI SCITVFFCGIVMSHYTWHNTESSRVTTKHAFAATLSFIA	313
		: :	

QY	313	ETFLFLYVGM	DALDIEKWEFASDRPGKSGISSILLGLVLICRAAFVFPPLSFISNLTKKA	372
dh	314	ETFLFLYVGM	DIEKWEFASDRPGKSGISSILLGLVLICRAAFVFPPLSFISNLTKKA	372

QY

373 PNEKITWRQQVVWAGLGRGVSIALAYNKFTRSHTQLHGNAIMTSTITVVFSTMV 432
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

[illegible]

DD 434 FGLMTEPLIRLLPHPRHHTNHILSDPSPKSLQPLLEEQQDSYADLVGPT-VPRPGS 492

QY 487 LRMLLTKPTHTVHYWYRKFDLALMRPMFCGRGFVPFSPGSPTEQS-HGGR 535

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Db      493  LRALLTPTHTVHYWRKFDFAFRPVFCGRGFAPFVPGSPTERSVRGGQ  542
RESULT 10

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Q9ZPK3 ID Q9ZPK3 PRELIMINARY; PRT; 538 AA.
AC Q9ZPK3;
01 MAY 1993

01-MAY-1999 (TReMBLrel. 10, Last sequence update)
01-JUN-2002 (TReMBLrel. 21, Last annotation update)
Sodium proton exchanger NHX1 (Fragment).

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
NH1. Embryophyta; Tracheophyta;

OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N A

STRAIN=CV. COLUMBIA;
MEDLINE=99145575; PubMed=9990049;
Gaxiola R.A., Rao R., Sherman A., Grisafi P., Alper S.L., Fink G.R.;

...the

function in cation detoxification in yeast.";
Proc. Natl. Acad. Sci. U.S.A. 96:1480-1485(1999).
[2]

RP SEQUENCE FROM N.A.
RA Quintero F.J., Blatt M.R., Pardo J.M.;
RT "The AtNH1 gene encodes a putative Na/H+ antiporter";
BT submitted to *M.P.*

DR EMBL; AF106324; AAD16946.1; -;
DR EMBL; AF056190; AAF21755.1; -;
DR InterPro; IPR001179; FKBP_ppiase.

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DR  INTERFIO; IPR004709; NAH_EXCHANGR.
DR  InterPro; IPR000676; NAH_Exchngr.
DR  Pfam; PF00999; Na_H_Exchange; 1.
DR  PRINTS; PR01084; NAHEXCHNGR.
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DR	TIGRFAMS; TIGR00840; b_cpai; 1.
DR	PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
FT	NON_TER 538 538
SO	SEQUENCE 538 AA: 59513 MW: 1189AD6C5C726996 CRC64.

Query Match	74.3%	Score 2023.5;	DB 10;	Leng
Best Local Similarity	73.3%	Pred. No. 2.5e-141;		
Matches	389.	Conservative	60.	Microbatch

QY 3 MEVAARLGALYTTSDYASVVSINLEVALLCACIVLGHLLLEENRWNESIT

Qy 63 VVLLMTKGSSHLFVFSEDLFFIYLLPPIIFNAGFQVKKKQFFERNFMTIT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

61 VTLLISKSGKSSHLLVFSEDLFFIYLLPPIFNAGFQVKRKKQGFERNFTVIL
QY 123 SFFTISAAIAIFSRMNI GTLDVGDFLAIGAIFSATDSVCTLQVLNQDETTP

DB 121 SCTIIISLGVTOFFKKLDIGTFDLGDLAIGAIFAATDSVCTLQVLNQDET
QY 183 GVVNDATSIVLFNALQNFDLVHIDAAVVLKFLGNFFYFLFSLSTFLGVFAGL

181	GVNDATSVVVFNAIQSFDLTHLNHEAAFHLLGNFLYFLFLLSTLLGAATGL
Db	
243	YGRHSTDREVALMMLMAYLSVMAELLDLSGILTVFFCGIVMSHYTWHNV
QY	

Db	241	YFGRHSTDREVALMMLMAYLSYMLAELFDLSGILTVFFCGIVMSHYTWHNV
Qy	303	HAFATLSFIAETFLFLYVGMDALDIEKWEFASDRPGKSGIGSSILLGLVLII

Db 301 HTEATLSFLAETFIFLYVGMDALIDKWRVSVDTPGTSIAVSSILMGLVMV
363 SFLSNLTKKAPNEKITWRQOVVWAGLMRGAVSIALAYNKETRSGHTQLHH
Qy

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361  SFLSNLAKKNQSEKINFNMQVVIWWSGLMRGAVSMALAYNKETRAGHTDVR
423  ITVVLFSTMVFGMMTKPLIRLLPASGHPVT--SEPSSPKSLHSPLITSMO

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421 1TVCLFSTVVFGLTKPLISYLLPHQNATTSMLSDDNTPKSIHPLLLDQDS
      |||||:||||:|||||||:|:|:||||:| |||
481 1VRPSSIRMI1TKPTHTVHVYWRKFDDA1MRPMEGGCGEVEFSPDCSPTEOS

```

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Db      : |||:| ||:| |||||:|:| ||:||||||| |||||:
481 VPRDSIRGFLTRPTRTVHYWYRQFDDSEMRPVFGGRGVFPVFGSPTRN

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RESULT 11	
Q94LX3	
ID Q94LX3	PRELIMINARY;
Q94LX3	PRT;
Q94LX3	555 AA.

DT	01-DEC-2001	(TREMBLrel. 19, Created)
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)

GN THPURPLE.
OS Torenia hybrida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Angiosperms; Eudicots; Rosales; Rubiales; Rubiaceae; Psychotriaceae; Psychotria

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; euasterids I; Lamiales; Lamiales incertae sed

GN NHX1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z., Zhang J., Chen S.;
RT "Isolation and characterization of two Na⁺/H⁺ antiporter genes from wheat.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY040245; AAK76737.1; -;
DR InterPro: IPR001179; FKBP_PP1ase.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR PROSITE: PS00453; FKBP_PP1ase.1; UNKNOWN.1.
SQ SEQUENCE 546 AA; 59704 MW; 45E1BCAB73E295C6 CRC64;

Query Match 70.6%; Score 1921.5; DB 10; Length 546;
Best Local Similarity 70.0%; Pred. No. 8.6e-134;
Matches 376; Conservative 64; Mismatches 88; Indels 9; Gaps 5;

QY 1 MGEVAAARLGALY- --TSDYASVVSINLFVALLCACIVLGHLLLEENRWVNESTALII 57
Db 1 MGLDGA --LAKYTGAVSDHDSIVAINFIALLCGCIVFGLHLLGNRWVNESTALIV 58

QY 58 GLCTGVILLMTKGSSHLVFSEDLFFIYLLPIIFNAGFQVKKQFFRNPMITILFGA 117
Db 59 GLITGGVILICTKGVNSRIIFSEDIFFIYLLPIIFNAGFQVKKQFFRNPMITILFGA 118

QY 118 VCTMSFETISAAIAIFSRMNICTLDVGDFLAIGAIFSDSVCTQLVNODEPFLYS 177
Db 119 AGTLISFVITFGMLFSKLDVGPLEGLDYLAIGAIFSDSVCTQLVNODEAPLIYS 178

QY 178 LVFEGGVNDATSIYFNALQNFVLHDAAVLKFGLNFFYLFSSSTFLGVFAGLLSAY 237
Db 179 LVFEGGVNDATSVYFNALQNFVLHDAAVLKFGLNFFYLFSSSTFLGVFAGLLSAY 238

QY 238 IIKLYIGRSTDRVALMMLMAYLSYMLAELDLGSLTVFFFCGIVMSHYTWHNVTESS 297
Db 239 IIKLCFAHSTDRVALMMLMAYLSYMLAELDLGSLTVFFFCGIVMSHYTWHNVTESS 298

QY 298 RVTKHAFATLSFAETFLYVGMADLDIEKWEFASDPGKSGICISILLGLVLIGRAA 357
Db 299 RVTKHAFATLSFAETFLYVGMADLDIEKWEFASDPGKSGICISILLGLVLIGRAA 358

QY 358 FVFPFLSLNLTKKAPNEKITRWQOVVITWAGLMRGAVSIALAYNKFTRSGHTOLHGNAI 417
Db 359 FVFPFLSLNLTSSKESHPKISFNQOVVITWAGLMRGAVSIALAYNKFTRSGHTAVRVNAV 418

QY 418 MITSTITVVFSTWVFGMMTKPLIRLLLPASGHPVTSPEPSKSLHSPLLTSMOGLS 477
Db 419 MITSTIIVVFSTWVFGMLTKPLINLIPP --RPGTAADISSQSFDPDLPTASLLGSDPD- 475

QY 478 TTNIVRPSLRMLTKPTHVTHYVWRKFDDALMRPMFGGRGVFPSPGSPTEQS-HG 533
Db 476 VQLTPTQNLQYLLTMTPTSRVHRVWRKFDDKFMRFMGGRGVFPVPGSPIERSVHG 532

RESULT 14
Q93YH2 ID Q93YH2 PRELIMINARY; PRT; 534 AA.
AC Q93YH2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Na⁺/H⁺ antiporter, isoform 1.
GN NHX1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RA Venema K., Belver A., Donaire J.;
RT "Cloning and characterization of two Na⁺/H⁺ antiporter isoforms from tomato.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ306630; CAC84522.1; -;
DR InterPro: IPR000676; NaH_Exchange.
DR Pfam: PF00999; Na_H_Exchange; 1.
SQ SEQUENCE 534 AA; 59037 MW; E4E736FA4A0C0791 CRC64;

Query Match 69.0%; Score 1879; DB 10; Length 534;
Best Local Similarity 68.8%; Pred. No. 1.1e-130;
Matches 369; Conservative 69; Mismatches 90; Indels 8; Gaps 5;

QY 1 MGEVAAARLG-ALYTTSDYASVVSINLFVALLCACIVLGHLLLEENRWVNESTALII 59
Db 1 MGLD- AVALRGVSIISDQSVSDSITLFAALLCGCIVLGHLLLEESRWINDSITLIVIGL 59

QY 60 CTGVILLMTKGSSHLVFSEDLFFIYLLPIIFNAGFQVKKQFFRNPMITILFGAVG 119
Db 60 STGGIILITTKGSSHLVEDEQLFFIYVLPPIIFNAGFQVKKQFFRNPMITILFGAVG 119

QY 120 TMISFETISAAIAIFSRMNICTLDVGDFLAIGAIFSDSVCTQLVNODEPFLYS 179
Db 120 TLISFISFGAKELDKLDIGLELDYLAIGAIFSDSVCTQLVNODEPFLYS 179

QY 180 FEGGVNDATSIYFNALQNFVLHDAAVLKFGLNFFYLFSSSTFLGVFAGLLSAY 239
Db 180 FEGGVNDATSVYFNALQNFVLHDAAVLKFGLNFFYLFSSSTFLGVFAGLLSAY 239

QY 240 KLYIGRSTDRVALMMLMAYLSYMLAELDLGSLTVFFFCGIVMSHYTWHNVTESS 299
Db 240 KLYIGRSTDRVALMMLMAYLSYMLAELDLGSLTVFFFCGIVMSHYTWHNVTESS 299

QY 300 TTGHAFATLSFAETFLYVGMADLDIEKWEFASDPGKSGICISILLGLVLIGRAAF 359
Db 300 TTGHAFATLSFAETFLYVGMADLDIEKWEFASDPGKSGICISILLGLVLIGRAAF 359

QY 360 FPLSFLSLNLTKKAPNEKITRWQOVVITWAGLMRGAVSIALAYNKFTRSGHTOLHGNAI 419
Db 360 FPLSFLSLNLTSSKESHPKISFNQOVVITWAGLMRGAVSIALAYNKFTRSGHTOLHGNAI 419

QY 420 TSTITVVFSTWVFGMMTKPLIRLLLPASGHPVTSPEPSKSLHSPLLTSMOGLS-ST 478
Db 420 TSTITVVFSTWVFGMLTKPLIRLLLPASGHPVTSPEPSKSLHSPLLTSMOGLS-ST 478

QY 479 TTNIVRPSLRMLTKPTHVTHYVWRKFDDALMRPMFGGRGVFPSPGSPTEQSHGG 534
Db 479 VDPVRPSGLSILLKPSYTIHNRWRFDADFMRLFGGRGVFPDAP----ELSKGG 530

RESULT 15
O04655 ID O04655 PRELIMINARY; PRT; 457 AA.
AC O04655;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE A_TM021B04.4 protein.
GN A_TM021B04.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Dante M., Wamsley P., Gibson A.;
RT "The sequence of A. thaliana TM021B04.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.


```
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Wash-U;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Waterston R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF007271; AAB61069.1; -.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR000676; NaH_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PROSITE; PS00453; FKBP_PPase_1; UNKNOWN_1.
SQ SEQUENCE 457 AA; 50611 MW; 0AF2F235F1A258EE CRC64;

Query Match 62.4%; Score 1698.5; DB 10; Length 457;
Best Local Similarity 74.0%; Pred. No. 2e-117;
Matches 333; Conservative 45; Mismatches 51; Indels 21; Gaps 3;

QY 3 MEVAARLGALYTTSDYASVSNLFAVALLCACIVLGHLLLENRWNNESITALLIGLCTG 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 LDSLVSKLPSL-STSDHASVVALNLFVALLCACIVLGHLLLENRWNNESITALLIGLCTG 60
QY 63 VVILLMTKCKSHLFEVSEDLFFIYLLPPIIFNAGFQVKKOFFRNFMTITLFGAVGTMI 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 VTILLISKGKSHLLVSEDLFFIYLLPPIIFNAGFQVKKOFFRNFMTITLFGAVGTII 120
QY 123 SPTTISIAAIAIFSRMNTGTLVDGFLAIGAIFSDTSVCTLQVLNQDETPLYSLVFE 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 SCTIISLGVTQFCKLDIGTFLDGLYLAIGAIFAATDSVCTLQVLNQDETPLYSLVFE 180
QY 183 GYVNDATSIIVLNALQNFEDLVHIDAAVVLKFLGNFFYFLSSTFLGV-----F 230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 GYVNDATSVVFNAIQSEDLTLNHEAAFHLLGNFLYLLSTLLGAASVPLFSSLPFFL 240
QY 231 AGLSAYIICKLYIG-----RHSTDREVALMMAYLSYMLAELDLGILTVFFCG 282
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 TGLISAYVIKKLYFGWPHINCHRHSTDRVALMMAYLSYMLAELDLGILTVFFCG 300
QY 283 IVMSHYTNHNVTESSRVTTKHAFTLSIAETFFLYVGMALDIEKWEFASDRPKSIG 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 IVMSHYTNHNVTESSRIITTKHTFATLSPLAETFFLYVGMALDIDKRSVSDTPTGTSIA 360
QY 343 ISSILGLVLIGRAAFVPLFLSNLTKKAPNEKITWQQQVVIWAGLMRGAVSTALAYN 402
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 VSSILMGLVYMGRAAFVPLFLSNLAKKNQSEKINFNQVVIWWSGLMRGAVSNALAYN 420
QY 403 KFRSGHTOLHGNAIMTITITVLFSTMV 432
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 KFRAGHTDVRGNAIMTITITVLCFSTVV 450
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Search completed: March 26, 2003, 18:53:48
Job time : 41 secs

